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Maximum Match 100%
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US-09-160-841-2
PCT-US94-05355-2
US-09-109-100-19
US-09-109-100-19
US-09-109-100-19
US-09-109-100-19
US-08-317-523A-9
US-08-439-818A-9
US-08-439-818A-9
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US-08-993-962-6
US-09-160-841-6
US-09-109-100-1
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US-07-756-250-16	PCT-US94-05150-12	US-08-933-803A-16	US-09-121-321-16	PCT-US93-02024-2	US-07-964-589-2	US-09-220-528-26	US-09-220-528-52	US-08-445-461-4	US-08-447-314-4	US-08-170-558-4	US-08-445-640-4	US-08-004-492-8	US-09-573-986-6	US-09-006-353A-6	US-08-808-599A-9	US-08-728-626-9	US-08-738-975-9
Sequence 16, Appl	•	Sequence 16, Appl	Sequence 16, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 26, Appl	Sequence 52, Appl	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 8, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 9, Appli	Sequence 9, Appli	Sequence 9, Appli

#### ALIGNMENTS

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RESULT 1
US-08-243-545-6
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                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
RAPPLICATION NUMBER: 0:
FILING DATE: May 24,
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Microsoft Word, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,545
FILING DATE: 11-MAY-1994
CLASSIFICATION: 435
                                                                                                                                CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REGISTRATION NUMBER: 28J
                                                                    TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 03-DEC-
APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lyman, Stewart D. APPLICANT: Beckmann, M. Patricia TITLE OF INVENTION: Ligands for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                          TELEFAX: (20
TELEFAX: 756822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 51 Univer:
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/106,463 FILING DATE: August 12, 1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                FILING DATE: August 25, 1993
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OPERATING SYSTEM: Macintosh
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ON: 435
TNTC: 1993
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Best Local Similarity
Matches 235; Conserv
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,962
                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/162,407
                                                    REFERENCE/DOCKET NUMBER: 2813-C TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,4
FILLION DATE: August 12, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,6
                                                                                                                                                               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: May 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/162,4
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIFICATION: 424
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CITY: Seattle
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51 University Street
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                                   (206) 587-0430
                                                                                                                                                         NUMBER: 08/068,394
May 24, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                 UMBER: US/08/993,962
December 18, 1997
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                                                                                    32,655
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RESULT 3
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Best Local S
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                                                                                                                                                         PRIOR APPLICATION NUMBER: 08/111/758

PRIOR APPLICATION DATA:
APPLICATION NUMBER
FILING PARTY.
                           REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                                                                           APPLICATION NUMBER: 08/06 FILING DATE: May 24, 1993 ATTORNEY/AGENT INFORMATION: NAME: Malaska, Stephen L.
                                                                                                                        APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
                                                                                                                                                                                                                                            CLASSIFICATION DATA:
PRIOR APPLICATION UNMBER: US/08/162,407
                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Microsoft Word, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lyman, Stewart D. APPLICANT: Beckmann, M. Patricia TITLE OF INVENTION: Ligands for
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                         MADLIUM TYPE: Floppy disk COMPUTER: Apple Macintosh OPERATING SYSTEM: Macintos SOFTWADER.
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TOPOLOGY:
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                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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o. 6190655
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              (206) 587-0430
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                          RESULT 5
PCT-US94-05365-6
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Best Local S
Matches 235
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CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 6, Application PC/TUS9405365 GENERAL INFORMATION:
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-THOMATTS AND METHODS OF
FILE REFERENCE: 03260.0028
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SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
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TYPE: ami
TOPOLOGY:
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Local Similarity 100.0%;
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Pred. No. 1.7e-117;
; Mismatches 0;
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Best Local S
Matches 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: May 11,
                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
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APPLICATION NUMBER:
FILING DATE: August
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/162,407
FILING DATE: December 3, 1993
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APPLICATION NUMBER:
FILING DATE: March 7
CLASSIFICATION:
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CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
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CITY: Seattle
STATE: Washing
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TELEFAX: 756822
 121
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                                                                                                                                                                               Local Similarity
nes 235; Conserv
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 RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT 180
                                                     ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL 120
                                                                                                        MTVLAPAWSPTTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
                                                                                                                           MTVLAPAWSPTTYLLLLLLLSSGLSGTQDCSFQHSPISSDEAVKIRELSDYLLQDYPVTV 60
                                    ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL 120
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GY: linear
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Beckmann, M. Patricia

WENTION: Ligands for flt3/flk-2 Receptors
                                                                                                                                                                                                                                                                                                                            235 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                 (206) 233-0644
                                                                                                                                                                           100.0%; Score 1242; DB 5; llarity 100.0%; Pred. No. 1.7e-117; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IUMBER: 08/111,758
August 25, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 August 12, 1993
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                                                                                                                 ; TYPE: PRT; ORGANISM: Homo sapiens US-09-109-100-18
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US-09-109-100-18
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SEQ ID NO 10
LENGTH: 212
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Patent No. 6291661
                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: MCGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 209
                                                                                                                                                                                                                                                                                                                                           Sequence 18, Application US/09109100C Patent No. 6291661
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Best Local
                                                              Query Match
Best Local 9
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
                                                  Matches
                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
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                                                 Watch 89.7%;
Local Similarity 100.0%;
nes 209; Conservative
               27 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL 86
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Application US/09109100C
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                                                                  Score 1114; DB 4;
Pred. No. 1.2e-104;
                                                  Mismatches
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GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
ITTLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF
FILE REFERENCE: 03560.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
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US-09-109-100-9
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; TYPE: PRT; ORGANISM: Homo sapiens US-09-109-100-12
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APPLICANT: Graddis, Thomas J.
APPLICANT: MCGrew, Jeffrey T.
APPLICANT: MCGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
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Best Local Similarity
Matches 208; Conserv
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CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
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TYPE: PRT
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                                            LENGTH: 209
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99.5%;
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APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF
FILE REFERENCE: 03360.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 198-07-02
NUMBER OF SEO ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
GENERAL INFORMATION:
APPLICANT: GEADDIS, Thomas J.
APPLICANT: McGrew, Jeffrey T.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260,0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
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Patent No. 6291661
GENERAL INFORMATION:
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                                                                                                 Sequence 17, Application US/09109100C
Patent No. 6291661
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                              208;
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APPLICANT: Graddis, Thomas J.
APPLICANT: MCGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109/100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 209
TYPE: PAT
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RESULT 13
US-09-109-100-15
; Sequence 15, Application
; Patent No. 6291661
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US-09-109-100-11
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SOFTWARE: PatentIn Ver. 7
SEQ ID NO 17
LENGTH: 209
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Best Local
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Local Similarity 99.5%;
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Pred. No. 4.8e-104;
1; Mismatches 0;
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Pred. No. 3e-104;
1; Mismatches
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APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOETWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 209
TYPE: PRT
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-13
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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Best Local Similarity 99.5%;
Matches 208; Conservative
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                                RQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLLPVGLLLLLAAAWCLH 206
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Pred. No. 6e-104;
0; Mismatches
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Pred. No. 4.8e-104;
0; Mismatches 1;
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CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
US-09-109-100-8
Search completed: November 24, 2002, 10:12:44 Job time: 15.1116 secs
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Best Local Sim
Matches 208;
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APPLICANT: MCGICW, Jeffrey T.
TITLE OF INVENTION: ELT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
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Pred. No. 7.6e-104;
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Database :
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2002 Compugen Ltd
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1544.781 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	σ	υī	4	ω	2	щ.		No.	Pacini+
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đ			hypothetical prote	probable beta-adap	apolipoprotein A-I	hypothetical prote	apolipoprotein A-I	A-	apolipoprotein A-I	hypothetical prote	hypothetical prote	leukosialin precur	zonadhesin - pig	colony-stimulating	macrophage colony-		peptidase, insulin	hypothetical prote	SERA antigen/papai	probable antigenic	hypothetical prote	ש	ligan	/FLK2 liga	ligand	flt3 ligand isofor	110	flt3/flk-2 ligand		Description	

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
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6.3	σ. ω	6.3	6.3	6.3	6.3	6.3	6.3	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4
619	811	774	774	746	579	456	266	1715	1601	908	806	743	224	3068	468
2	N	N	Ŋ	N	N	N	N	N	2	N	N	2	N	۲	N
D86509	E72003	H81540	в86492	S67203	JC7629	в72130	A45844	T06145	AE2011	S51293	E64221	T34632	I37243	A44062	T23091
S/T protein kinase	hypothetical prote	hypothetical prote	hypothetical prote	probable membrane	membrane-type friz	frame-shift with c	MHC class II histo	disease resistance	hypothetical prote	probable membrane	phenylalanine-tRNA	probable bi-functi	CMRF-35 antigen -	genome polyprotein	hypothetical prote

### ALIGNMENTS

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flt3/flk-2 ligand precursor - mouse
c;Species: Mus musculus (house mouse)
c;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
C;Accession: A49265; I49347; I49346; S43290
R;Lyman, S.D.; James, L.; Vanden Bos, T.; de Vries, P.; Brasel, K.; Gliniak, B.; Holl D.; Williams, D.E.; Beckmann, M.P.
Cell 75, 1157-1167, 1993
                                                                                                                                                                                                                                                                                                                                                                                                          A;Introns: 11/3; 49/3; 67/3; 115/3; 164/1; 224/3 C;Keywords: transmembrane protein
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A; Residues: 1-197,'1,',198-231 <RE2>
A; Residues: 1-197,'1,',198-231 <RE2>
A; Residues: 1-197,'1,',198-231 <RE2>
A; Construction: The control of the
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     В
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A; Residues: 1-197, 'L', 198-231 <HAN>
A; Experimental source: clone T110
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A;Molecule type: DNA
A;Residues: 1-163,'G',165,'HYAG' <RES>
A;Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90952.1; PID:g1072041
A;Accession: 149346
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A; Residues: 1-231 <LYM>
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Best Local
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                                                       1 MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT 60
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MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
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Pred. No. 2.9e-101;
                                                                                                                                                                                                                   Mismatches
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A;Tille: Identification of soluble and membrane-bound isoforms of the murine A;Reference number: 158343; MUID:95124710; PMID:7824267
A;Accession: I58343
                                 Qy
                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-220 <RES>
A;Cross-references: GB:S76459; NID:g913479; PIDN:AAB33069.1; PID:g913480
                                                                                                                                                                                                                                                                                                   C;Species: Mus sp. (mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C;Accession: I58343
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A;Molecule type: mRNA
A;Residues: 1-220 <HAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates A; Reference number: S43290; MUID:94195428; PMID:8145851 A; Accession: S43291
                                                                                                                                                                                                                                                                                                                                                         flt3 ligand isoform 5H - mouse
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1 MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
                                                                    Local Similarity
nes 177; Conserv
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                                                                       Conservative
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82.3%;
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82.3%;
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                                                                                   Score 879; DB 2
Pred. No. 1e-70;
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Pred. No. 1e-70;
                                                                      Mismatches
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138440
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A; Residues: 1-235 < RES>
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                                                                                                                                                                                                                                                                                                                                        Similarity
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A; Molecule type: mRNA
A; Residues: 1-71, 'A', 73-235 <HAN>
A; Residues: 1-71, 'A', 73-235 <HAN>
A; Cross-references: GB:U04806; NID:g483844; PIDN:AAA17999.1; PID:g483845
A; Cross-references: GB:U04806; NID:g483844; PIDN:AAA17999.1; PID:g483845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:U29874; NID:g1072036; PIDN:AAA90949.1; PID:g1072037
R;Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, felt, A.; Muench, M.; Kelner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zl Mature 368, 643-648, 1994
A;Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haema A;Reference number: S43290; MUID:94195428; PMID:8145851
A;Accession: S43292
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C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change
C;Accession: I38440; I39075; e43292
R;Lyman, S.D.; James, L.; Johnson, L.; Brasel, K.; de Vries, P.;
Blood 83, 2795-2801, 1994
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A;Molecule type: DNA
A;Residues: 1-235 <RE2>
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VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEATELPEPRPRQLLLL-----LLLLPLTLVLLAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11/3; 48/3; 66/3; 114/3; 161/1; 220/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.8%; Score 768.5; DB 2; 70.3%; Pred. No. 7.1e-61; tive 17; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K.; de Vries, P.; Escobar, S.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9,
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                                                                                                     177
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C:Species: Homo Sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C:Accession: I39076
R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar Oncogene 11, 1165-1172, 1995
A:Title: Structural analysis of human and murine flt3 ligand genomic loci.
A:Reference number: I39075; MUID:96032581; PMID:7566977
A:Accession: I39076
A:Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                               A;Cross-references: EMBL:U29874; NID:g1072036; PIDN:AAA90950.1; PID:g1072038 C:Genetics: A;Introns: 11/3; 48/3; 66/3; 114/3; 161/1
                                      Ωy
                                                                                                               9
                                                                                                                                                                                                                                                                                            A:Status: preliminary: translated from GB/EMBL/DDBJA;Molecule type: DNAA;Residues: 1-178 <RES>
      ₽
                                                                               망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Flt3 ligand alternatively spliced isoform - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-245 <HAN>
A;Note: the authors translated the codon AGT for residue 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoieti
A;Reference number: $43290; MUID:94195428; PMID:8145851
A;Accession: $43293
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C;Accession: S43293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLT3/FLK2 ligand
                                                                                                                                                        Query Match
Best Local S
Matches 120
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Best Local
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    60
                                        61
                                                                                                                                                                            Local Similarity
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                                                                                                                     \vdash
                    VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
                                                                                               MTVLAPAWSPNSSLLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT 60
                                                                         IPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MTVLAPAWSP-TTYLLLLLLLSSGLMGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVT 59
VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TWPRPHPGEDTEAHRGESPARGCI----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VASNLQDEELCGALWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHEVTKCAFQPPPSC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           i (clone S109) -
sapiens (man)
                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                          48.6%;
73.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.4%; Score 616.5; DB 2 57.0%; Pred. No. 2.4e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RQLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPL 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                        14;
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                                                                                                                                                    Score 594.5; DB 2;
Pred. No. 1.5e-45;
4; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anahan, T.; Zurawski, S.; Bazan, J.F.;
Rennick, D.; Roncarolo, M.G.; Zlotnik,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -AW---TQRKLARGRSLPWAPL 218
                                                                                                                                                      Indels
                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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                                                                           59
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RESULT T01438

8

hypothetical protein GS034D21.1 - human (fragment)

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A;Note: F20B18.200
C;Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein rep
C;Keywords: leucine zipper; membrane protein; nucleotide binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell 78, 1089-1099, 1994
A;Title: The Arabidopsis thaliana disease resistance gene A;Reference number: A54809; MUID:95007758; PMID:7923358
A;Accession: A54809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C:Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 20-Apr-2000
C;Accession: A54809; A54811; T04264
R;Mindrinos, M.; Katagiri, F.; Yu, G.L.; Ausubel, F.M.
Cell 78, 1089-1099, 1994
밁
                                      QΥ
                                                                                                                                QΥ
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                                                                                                                                                                                                                              Qy
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                                                                                         Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                 Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: cultivar Columbia; C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A: Residues: 1-909 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; not
A;Molecule type: DNA; mRNA
A;Residues: 1-909 <BEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: RPS2 of Arabidopsis thaliana: a leucine-rich repeat class of plant disease r A;Reference number: A54811; MUID:94377978; PMID:8091210 A;Accession: A54811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:U12860; NID:g549978; PIDN:AAA50236.1; PID:g549979 R;Bent, A.F.; Kunkel, B.N.; Dahlbeck, D.; Brown, K.L.; Schmidt, R.; Giray Science 265, 1856-1860, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease resistance protein RPS2 - Arabidopsis thaliana N; Alternate names: protein F20B18.200 \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: EMBL: AL049483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-909 <MIN>
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Best Local
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                                      209 G
763
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                                                                                                                                149 ACQNFSRCLEVQCQPDSSTLLPPRSPIALEATELPEPRPRQLLLLLLLLLLLLLLLAAAW 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQP
                                                                                    715 HGRNLRR-LSIKSCHDLEYLV---TPADFENDWLPS---LEVLTLHSLHNLTRV-----W
                                                                                                                                                                                                                                                                         595 VLPQELGNLRKLKHLDLQRTQFLQTIPRDAICWLSKLEVLNLYYSYAGWELQSFGEDEAE
                                                                                                                                                                                                                                                                                                                            63
                                                                                                                                                                                                                                                                                                                                                                                                              14 LLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTD-----HLLKDYPVTVA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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o -
                                                                                                                                                                                                                                   EIHF----
                                                                                                                                                                                                                                                                                                                                                                LTTLMLQQNSSLKKIPTGFFMHMPVLRVLDLSFTSITEIPLSIKYLVELYHLSMSGTKIS
                                                                                                                                                                                ELGFADLEYLENLTTLGITVLSLETLKTLFEFGALHKHIQHLHVEECNELLYFNLPSLTN 714
                                                                                                                                                                                                                                                                                                                     -----VNLQDEKHCKALWSLFL-----AQRWIEQLKTV-----AGSKMQTLLEDVNT
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                                           209
763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                            ------VTSCTFQPLPECLRF--VQTNISHLLKDTCTQLLALK-PCIGK 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.8%;
22.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 95.5;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163
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C;Geneti
A;Gene:
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R;Parkhill, J:; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
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    Db
Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable antigenic leucine-rich repeat protein YPO1006 [imported] - Yersinia
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
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A; Accession: T01438
A; Status: preliminary; translated
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C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 05-Nov-1999
C;Accession: T01438
R;Smith, A.; Harmon, G.; Elliott, G.; Twyman, B.
                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-291 <KI
                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: AB0001; A; Accession: AF0123
                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Genome sequence of Yersinia pestis, the causative agent of plague A; Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Note: intron positions not resolved (incomplete A; Note: WUGSC:H\_GS034D21.1
                                                                                                                                                                                                                                                                                          A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:AC003077; NID:g2588634; PIDN:AAB83946.1;
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A; Residues: 1-843 <SMI>
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                                        1,99 VTSCTFQPLPE----C--LRFVQTNISHL------LKDTCTQLLALKPCIGKACQN 152
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LSSLDLTSLPDTLPPCNELNIICNNLTELPTTLPDNLQTLKASYNQLRTLPNTLPASLLS
                                                                                                             DYPVTVAVNLQDEKHCKALWSLFLAQRWIEQLKTVAG---
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                                                                               DRPAATALTPAD---YHAIW-----EKWENDPRTVAGEQRGQAVARMKECLEN-NAERLN 74
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                                                                                                                                                                                       Similarity
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Pred. No.
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November 1997
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RESULT 11
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C71617
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                                                                                                                                                                                                                                                                                                                                                         hypothetical protein D1086.1 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t
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                                                                                                     A; Map position: 5
A; Introns: 112/3; 132/3;
                                                                                                                                             A; Gene: CESP: D1086.1
                                                                                                                                                                               A;Cross-references: EMBL:Z81491; PIDN:CAB04019.1; GSPDB:GN00023; CESP:D1086.1 A;Experimental source: clone D1086
                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-181 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: C71617
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                                 . Similarity 39; Conserv
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                                 Conservative
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                              b; Score 85; DB
b; Pred. No. 2.8;
24; Mismatches
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                                                                                                                                                                                                                                                                                                            November 1996
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13 SLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKD----

-YPVTVAVNLQD

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RESULT 12
E82121
peptidase,
C; Species:
                                                                                                                        presynaptic activity regulator aex-3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 03-Dec-1999 *sequence_revision 03-Dec-1999 *text_chance_caecesion: T37188 R;Leinbac, D.; Minx, M.
submitted to the EMBL Data Library, Februa
A;Description: The sequence of C. elegans
A;Reference number: 120523
A;Accession: T37188
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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C; Superfamily:
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A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-939 <HEI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: DNA Sequence of both chromosomes of the cholera A; Reference number: A82035; MUID:20406833; PMID:10952301 A; Accession: E82121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, N. R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: E82121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 LKTVAGSKMQTLLEDVNTE--IHFVTSCTFQ------PLPECLRFVQTNISHLLK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 SNFKVKFRELTDHLLKDY-----PVTVAV-----NLQDEKHCKALWSLFLAQRWIEQ 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 TILPELLELSKAENSPLDCSKDDLQLTVTCRPKLAKLTDEMKKNPLNSGEPSVETLN-KM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DALRYQGQTYEESLRPLYMLGKS-GTFQR--EVQCQQDDSAIVVYYQSHEVSPRS-IALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DTC-----TQLLALKPCI--GKACQNFSRCLEVQCQPDSSTL------LPPRSPIAL- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PNNPPYAELLAAIDDVQVEELAHFVDTILSQLHVEMFVYGDWPAAEAHK-----MAEVLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGFSQKLPQLMEVILRKFAQRDFQPKRFATIKQQMTRNWRNAAHDKPISQLFNAMTGLLQ 646
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Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61;
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Pred. No. 20;
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H.; Dragoi, I.; Sellers,
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A;Residues: 33-39, CC7,42-57 <BEN>
R;Rejavashisth, T.B.; Eng, R.; Shadduck, R.K.; Waheed, A.; Ben-Avram, C.M.; Shively, Proc. Natl. Acad. Sci. U.S.A. 84, 1157-1161, 1987
A;Title: Cloning and tissue-specific expression of mouse macrophage colony stimulatin A;Reference number: A25883; MUID:87147232; PMID:3493488
                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-5, K',7-245, 'A',247-552 <DEL>
R; Ben-Avram, C.M.; Shively, J.E.; Shadduck, R.K.; Waheed,
Proc. Natl. Acad. Sci. U.S.A. 82, 4486-4489, 1985
Proc. Natl. Acad. Sci. U.S.A. 82, 4486-4489, 1985
A; Reference number: A23166; MUID:85242709; PMID:3925458
                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M81316; GB:M61708; NID:g192802; PIDN:AAA19866.1; PID:g192803 R;DeLamarter, J.F.; Hession, C.; Semon, D.; Gough, N.M.; Rothenbuhler, R.; Mermod, Nucleic Acids Res. 15, 2389-2390, 1987 Nucleic Acids Res. 2390, 2390, 1987 A;Title: Nucleotide sequence of a cDNA encoding murine CSF-1 (macrophage-CSF). A;Reference number: A26575; MUID:87174763; PMID:3494232 A;Accession: A26575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene 102, 165-170, 1991
A;Title: Cloning and characterization of the murine promoter A:Reference number: JNO294; MUID:91340149; PMID:1874443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         macrophage colony-stimulating factor precursor N; Alternate names: colony-stimulating factor 1; 1 C: Species: Mus musculus (house mouse)
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A;Cross-references: EMBL:U49945; PIDN:AAC47926.1; GSPDB:GN00029
A;Experimental source: strain Bristol N2; clone C02H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M21952; GB:J03862; NID:g192804; PIDN:AAA37481.1; R;Harrington, M.A.; Edenberg, H.J.; Saxman, S.; Pedigo, L.M.; Daub, R.; Gene 102, 165-170, 1991
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A; Residues: 1-13 <HAR>
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A; Accession: JN0294
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A; Residues: 1-552 <LAD>
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                                                                                                            A; Molecule type: protein A; Residues: 33-39, 'CC', 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLPAYMPSAE--QLLLAPTPFLIGVPSSFFHHR------KIRELPSDVILVDLD-TNC 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LQVPDD-----LYIPDLPEPDATHLKERLKN-AINKMTTMTVDNETSVTDADFGIDI 416
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B.; Martin, G.A.; Noble, J.A.; Wittman, V.P.;
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Pred. No.
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A;Cross-references: GB:M15692; NID:g192800; PIDN:AAA37480.1; PID:g192801

'RPR',9-100 <RAJ>

A; Molecule type: mRNA A; Residues: 1-2,4-5,' A; Accession: A25883

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C;Superfamily: macrophage colony-stimulating factor C;Keywords: cytokine; glycoprotein; growth factor; macrophage F;1-32/Domain: signal sequence #status predicted <SIC> F;33-552/Product: macrophage colony-stimulating factor #status predicted <MAT> F;154,172/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Colony-stimulating factor - rat
C.Species: Rattus norvegicus (Norway rat)
C.Species: Rattus norvegicus (Norway rat)
C.Depcies: Rattus norvegicus (Norway rat)
C.Accession: 335703
C.Accession: 335703
C.Accession: 335703
A.F.; Guillier, M.; Leibovitch, S.A.
Biochim. Biophys. Acta 1174, 143-152, 1993
A.FItle: Isolation and characterization of a cDNA clone encoding for rat CSI
A.Reference number: S35703; MUID:93363632; PMID:8357831
A.Reference number: S35703; MUID:93363632; PMID:8357831
A.Recession: S35703
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-552 cBOR>
A.Residues: 1-552 cBOR>
A.Residues: 1-552 cBOR>
A.Residues: 1-552 cBOR>
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Local Similarity 23.2%;
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YA4G_SCHPO
YM72_MYCTU
RCQ4_HUMAN
POLG_PEMVC
CM35_HUMAN
POLG_PEMVC
RMT
HB2D_CANFA
GBR2_RAT
YB95_ROTS1
ASA1_ENTFA
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ATS3_HUMAN
AEX3_CAEEL
CSF1_MOUSE
ZAN_PIG
       DMD_CHICK
PRI1_DROME
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CYB_CAMDR
TRBM_MOUSE
LRP1_CHICK
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Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC
CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULAT.
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BL; U29875; AAA390951.1; -.
BL; S76459; AAB33069.1; -.
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BL; S76464; AAB3307.1; -.
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BL; U44024; AAA93306.1; -.
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SUBUNIT: Homodimer (soluble isoform) (By similarity).

SUBCELLULAR LOCATION: Type I membrane protein. Two soluble isoforms are also produced by alternative splicing. One of which, isoform 3/E6, is biologically active, while the other, isoform 4/E6Delta16, is inactive.

ALTERNATIVE PRODUCTS: 4 isoforms; 1/6C (shown here), 2/5H, 3/E6
                                                                                                                            ELPEPRPRQ-LLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP
                                                                                        VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                        LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
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                           LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
                                                                            VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collabeen the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00947; flt3_lig; 1.
PF00947; flt3_lig; 1.
Inc. Glycoprotein; Transmembrane; Alternative splicing; Signal.
                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4/E6Delta16; are produced by alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR004213;
                                                                                                                                                                                                                               141
198
232
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                  164
170
159
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190
211
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31
71
120
127
152
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26141
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112
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1527
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99.6%;
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                                                                                                                                                                                                                                   , WM
                                                                                                                                                                                                                                                                                                                           POTENTIAL.

CYTOPLASMIC (POTENTIAL).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).

LAAAWGIRWQRARRRGELHPEPERRQLLLLLLLLLEUTUL

LAAAWGIRWQRARRRGELHPGVPLPSHP -> GNGGPRAQH

HGATRLTATALLTVCPGLLLPLVGTSHMFFLLPYFLSF
                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
SL CYTOKIN
                                                                                                                                                                                            Score 1212.5;
Pred. No. 3.1
                                                                                                                                                                                                                                            VQCQP -> GLIMOARLTLNSKQSSCLSVLSAGIT ISOFORM 4).
A -> G (IN REF. 1).
MISSING (IN REF. 2).
                                                                                                                                                                                                                                                                                             DSSTLL -> GSHYAG (IN ISOFORM MISSING (IN ISOFORM 3).
                                                                                                                                                                                                                                                                                                       LKMYLYV (IN ISOFORM 2)
DSSTLL -> GSHYAG (IN I
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                 3A3680D3CB69FBA6
                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                            le-99
                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Usage
                                                                                                                                                                               0;
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Db 181 ELPEPRPRQLLLLLLLLLLPLTLYLLAAAWGLRWQRARRRGELHPGVPLPSHP 232
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RESULT 2

RESULT 2

FIST HUMAN

FIST HOMO

FIST
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01-OCT-1996 (Rel. 34, 1
15-JUN-2002 (Rel. 41, 1
SL cytokine precursor (
ligand) (Flt3L).
                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bundles and cystine knots.";
Nat. Struct. Biol. 7:486-491(2000).

-i-FUNCTION: STIMULATES THE PROLIFERATIO
CELLS. SYNERGIZES WELL WITH A NUMBER
FACTORS AND INTERLEUKINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lyman S.D., James L., Johnson L., Brasel K., de Vries P., Escobar S.S., Downey H., Splett R.R., Beckman M.P., McKenna H.J.; "Cloning of the human homologue of the murine flt3 ligand: a growth factor for early hematopoletic progenitor cells."; Blood 83:2795-2801(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94195428; PubMed=8145851; Hannum C., Culpepper J., Campbell D., McClanahan T., Zurz Hannum C., Culpepper J., Campbell D., Magner J., Mattson J. Bazan J.F., Kastelein R., Hudak S., Wagner J., Mattson J. Duda G., Martina N., Peterson D., Menon S., Shanafelt A., Muench M., Kelner G., Namikawa R., Rennick D., Roncarolo Zlotnik A., Rosnet O., Dubreuil P., Birnbaum D., Lee F.; "Ligand for FLT3/FLK2 receptor tyrosine kinase regulates haematopoietic stem cells and is encoded by variant RNAs. Nature 368:643-648(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCULIT: Homodimer (isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Savvides S.N., Boone T., Karplus P.A.; "Flt3 ligand structure and unexpected commonalities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20343011; PubMed=10881197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FL3L_HUMAN P49771;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oncogene 11:1165-1172(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lyman S.D.,
Escobar S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., MEDLINE=96032581; P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                     secreted (isoform 2).
ALTERNATIVE PRODUCTS: 2 isoforms; a and 2/soluble; are produced by alter
                              U04806; AAA17999.1; -. U03858; AAA19825.1; -. U29874; AAA90949.1; -. U29874; AAA90950.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     analysis of human and murine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          K., Davison B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
(Fms-related tyrosine k
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                                                                                                                                                                                                                                                                                                                                                                        alternative splicing.
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                                                                                                                                                                                                                                                                                                                                                                                                    1/membrane-bound
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Johnson L.,
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on J., Lub
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L outstation -
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GBR2_HUMAN
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Best Local
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DISULFID
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CARBOHYD
                                                                                                                                                                                                                          Gamma-aminobutyric acid type B receptor, subunit 2 receptor 2) (GABA-B-R2) (Gb2) (GABABR2) (G protein-51) (GPR 51) (HG20).
                                                                                                                                                                                                                                                                                              GBR2_HUMAN STANDARD; PRT; 94:
075899; 075974; 075975; Q9UNS9; Q9UNR1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
MEDLINE=20193514; PubMed=10727622;
Clark J.A., Mezey E., Lam A.S., Bonner T.I.;
"Distribution of the GABA(B) receptor subunit gb2
                                                                                       White J.H., Wise A., Main M.J., Gree Barnes A.A., Emson P., Foord S.M., 1 "Heterodimerization is required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3D-structure.
                                                                   GABA(B) receptor.";
Nature 396:679-682(1998).
                                                                                                                                     SEQUENCE FROM N.A. TISSUE=Cerebellum;
                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                   TISSUE-Brain;
                                             PARTIAL SEQUENCE FROM
                                                                                                                       MEDLINE=99087321; PubMed=9872316;
                                                                                                                                                                    NCBI_TaxID=9606,
                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                178
                                                                                                                                                                                                                                                                                                                                                                                     181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; HGNC:3766; FLT3LG. 600007; -.
                                                                                                                                                                                                                                                                                                                                                                APTAPQPP---LLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSP
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                                                                                                                                                                                                                  OR GPR51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                               Eutheria; Primates;
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G -> A (IN REF. 1).
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CYTOPLASMIC (POTENTIAL)
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N-LIMED (GLCNAC. ..) (POTENTIAL).
DSSTLPPPWSPRPLEATA -> VETVFHRVSQDGLDLLTS
(IN ISOFORM 2).
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SL CYTOKINE
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                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73B95BF693B4CECF CRC64;
                                                                                        Green A., Fraser N.J., M., Marshall F.H.; for the formation of a
                                             2A;
                                                                                                                                                                                                                                                                                              11 AA.
Q9P1R2;
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                                                                                                                                                                                                                                      ubunit 2 precursor (GABA-B protein-coupled receptor
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   rat CNS.
                                                                                                                Disney G.H.,
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Sullivan R., Chatcauneuf A., Coulombe N., Kolakowski L.E. JI., Sullivan R., Chatcauneuf A., Coulombe N., Kolakowski L.E. JI., Johnson M.P., Hebbert T.E., Ethier N., Belley M., Metters K., Abramovitz M., O'Neill G.P., Ng G.Y.K.;

"Coexpression of full-length gamma-aminobutyric Acid(B) (GABA(B)) receptors with truncated receptors and metabotropic glutamate receptor 4 supports the GABA(B) heterodimer as the functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning and characterization of a novel human GABA-B receptor subtype with high affinity for GABA and low affinity for baclofen."; submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ng G.Y.K., Clark J., Coulombe N., Ethier N., Hebert T.E., Sullivan Kargman S., Chateauneuf A., Tsukamoto N., McDonald T., Whiting P., Mezey E., Johnson M.P., Liu Q., Kolakowski L.F. Jr., Evans J.F., Bonner T.I., O'Neill G.P., Bonner T.I., O'Neill G.P., "Identification of a GABAB receptor subunit, gb2, required for functional GABAB receptor activity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning of a novel G-protein-coupled receptor GPR 51 resembling receptors expressed predominantly in nervous tissues and mapped proximal to the hereditary sensory neuropathy type 1 locus on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O'Neill G.P., Liu Q.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JAN-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Hippocampus;
Borowsky B., Laz T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brain Res. 860:41-52(2000)
[3]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99189236;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GABABR1."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Martin S.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99263199; PubMed=10328880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Brain
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                                                                                                                                                                                                                                                                                                                            J. Pharmacol. Exp. Ther.
                                                                                                                                                                                                                                                                                                                                            receptor."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20237752; PubMed=10773016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R1A-R2 INTERACTION.
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                                                                             INOSITOL PHOSPHOLIPIDS HYDROLYSIS, PLAYS A CRITICAL ROLE IN THE FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN SYNAPTIC INHIBITORY DOSTSYNAPTIC OTHERNAL LONG-TERM SYNAPTIC INHIBITON BUT ALSO IN HIPPOCAMPAL LONG-TERM SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM SYNAPTIC TOTERNAL SUNGSCLE RELAXATION AND
                                                                                                                                                                                                                                                  Pharmacol. Exp. Ther. 293:460-467(2000).
FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G-PROTEINS THAT INHIBITS ADENVLYL CYCLASE ACTIVITY, STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS, INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES
                                ANTINOCICEPTION.
SUBUNIT: HETEROL
IS EFFECTIVE ON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ., Russek S.J., Farb D.H.; identification of the human GABABR2: and coupling to adenylyl cyclase in
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                                HETERODIMER OF
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nald T., Bonnert T., Rigby M., Heavens R.,
Coulombe N., Kargman S., Caskey T., Evans
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McCrea K., Watson J.,
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EMBL/GenBank/DDBJ databases
                                GABA-B-R1 AND GABA-B-R2. AND HOMODIMERIC ASSEMBLY
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SUBCELLULAR LOCATION:

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TRANSMEM
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InterPro; IPR001377; GPCR_Mgr.
Pfam; PF00003; 7tm_3; 1.
Pfam; PF01004; ANF_receptor; 1.
PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; FALSE_NEG.
PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; FALSE_NEG.
PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; FALSE_NEG.
PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; FALSE_NEG.
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L; AF055085; AAC63228.1;
L; AF095723; AAC63383.1;
L; AF095724; AAC63384.1;
L; AF095784; AAD30389.1;
L; AF074483; AAD03336.1;
L; AF069755; AAC99345.1;
L; AF069755; AAC99345.1;
L; AF099033; AAD45867.1;
L; AF099047.1; AAD45867.1;
L; AF099047.1; AAD45867.1;
L; AF099047.1; AAD45867.1;
L; AF099047.1; 
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TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN, ESPECIALLY IN CREBRAL CORPEX, THALAMUS, HIPPOCAMPUS, FRONTAL, OCCIPITAL AND TEMPORAL LOBE, OCCIPITAL POLE AND CEREBELLUM, FOLLOWED BY CORPUS CALLOSOM, CAUDATE NUCLEUS, SPINAL CORD, AMYGDALA AND MEDULLA.

WEAKLY EXPRESSED IN HEART, TESTIS AND SKELETAL MUSCLE.

DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 1.

SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GABA-B RECEPTOR SUBFAMILY.
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ALTERNATIVE PRODUCTS:
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; PS50259;
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                                                                                                                      membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO
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504
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ptor; Transmembrane; Glycoprotein; Signal;
Coiled coil; Alternative splicing;
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VI (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

VII (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

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N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).

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III POTENTIAL.
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(ED (GLUNAC. . .) (POTENTIAL).

KED (GLUNAC. . .) (POTENTIAL).

NG (IN ISOFORM 2B).

PERVMVSGL -> TILGRGVCCRNTVGSGCGEAGHHG

PERVMVSGL (IN ISOFORM 2C).
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O88839; Q9QYL2;
16-OCT-2001 (Re:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Howard L., Nelson K.K., Maciewicz R.A., Blobel C.P., "Interaction of the metalloprotease disintegrins MDC two SH3 domain-containing proteins, endophilin I and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Myeloid, and Myeloma;
Shimizu E., Higuchi Y., Matsuura K., Hijiya N., Yamamoto
"Structure of the mouse ADAM 15 (AD56) gene.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98421554; PubMed=9748307;
Lum L., Reid M.S., Blobel C.P.;
"Intracellular maturation of the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERACTIONS WITH ENDOPHILIN I AND SORTING MEDLINE=20002705; PubMed=10531379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa: Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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15-JUN-2002 (Rel. 41, Last annotation update)
ADAM 15 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase domain 15) (Metalloproteinase-like, disintegrin-like, and cysteine-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MDC15
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15-JUN-2002 (Rel.
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(Rel. 10,
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49.0%;
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S -> R (IN REF. 5).
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G -> E (IN REF. 3).
MW; 09F1773DB0673C5D C
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SORTING NEXIN 9.
DOMAIN: DESINTEGRIN

PRECURSOR

IS CLEAVED BY A FURIN ENDOPEPTIDASE. AN

THE

CYTOPLASMIC DOMAIN INTERACTS WITH

DOMAIN BINDS

TO

INTEGRIN ALPHAV-BETA3 (BY

ENDOPHILIN I AND

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InterPro; IPR001762; Disintegrin.
InterPro; IPR000561; EGF-like.
InterPro; IPR001818; Matrixin.
InterPro; IPR002870; Pep_M12B_propep.
InterPro; IPR001590; Reprolysin.
InterPro; IPR00130; Zn_MTpeptdse.
InterPro; IPR000130; Zn_MTpeptdse.
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                                                                                                                                                                                                                                        METAL
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PROSITE; PS00022; EGF_1; FALSE.N
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS00427; DISINTEGRIN_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AB022089; BAA88903.1; HSSP; P17494; 1KST.
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PROSITE; PS00546; CYSTEINE_SWITCH;
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SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
SIMILARITY: CONTAINS 1 DEF-LIKE DOMAIN.
SIMILARITY: CONTAINS 1 DISINTEGRIN DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
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PS01186; EGF_2; 1.
PS00427; DISINTEGRIN_1; FALSE_NEG.
PS50214; DISINTEGRIN_2; 1.
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CYSTEINE SWITCH.
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16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
ADAM 15 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase domain 15) (Metalloproteinase like, disintegrin-like, and cysteine-rich protein 15) (MDC-15) (Metalloprotease RGD disintegrin protein)
(Metargidin) (CRII-7).
ADAM15 OR MDC15.
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                                                                                                                                                                                         Rattus norvegicus (Rat).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                           TISSUE=Sciatic
                                                                                                                                                                  SEQUENCE FROM N.A.
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PROSITE; PS50215; ADAM_MEPRO; 1.

PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.

R PROSITE; PS50214; DISINTEGRIN_2; 1.

R PROSITE; PS00122; EGF_1; FALSE_NEG.

R PROSITE; PS001186; EGF_2; 1.

R PROSITE; PS00142; ZINC_PROTEASE; 1.

PROSITE; PS00142; ZINC_PROTEASE; 1.

PROSITE; PS00546; CYSTEINE_SWITCH; FALSE_NEG.

PROSITE; PS00546; CYSTEINE_SWITCH; Gl
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INDUCTION: IN RESPONSE TO SCIATIC NERVE INJURY
DOMAIN: THE CYTOPLASMIC DOMAIN INTERACTS WITH I
SORTING NEXIN 9 (BY SIMILARITY).
DOMAIN: DESINTEGRIN DOMAIN BINDS TO INTEGRIN AI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00200; disintegrin; 1.
PF01421; Reprolysin; 1.
PF01562; Pep_M12B_propep; 1.
m; PD000664; Disintegrin; 1.
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         ike domain; SH3-binding
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SH3-BINDING (POT
CYSTEINE SWITCH.
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POLY-LEU.
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BY SIMILARITY.
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Signal; Glycoprotein; Zymogen;
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                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
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RESULT 6
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                                                                                                                                                                     Nagase T., Ishikawa K. I., Nakajima D., Ohira M., Seki Miyajina N., Tanaka A., Kotani H., Nomura N., Ohara O., Precipita N., Tanaka A., Kotani H., Nomura N., Ohara O., Precipita N., Tanaka A., Kotani H., Nomura N., Ohara O., Precipita N., Tanaka A., Kotani H., Nomura N., Ohara O., Precipita N., Kotani H., Nomura N., Ohara O., Precipita N., Nomura N.,
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Best Local
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015072; Q9BXZ8;
16-OCT-2001 (Rel. 40, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADAMTS-3 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 3) (ADAM-TS 3) (ADAM-TS 3) (Procollagen II
                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97349984; PubMed-9205841;
Nagase T., Ishikawa K.-I., Nakajima
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 5-1205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eyre D.R., Apte S.S., "Procollagen II amino dermatosparaxis.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21402912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dermatosparaxis.
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SIMILARITY).
SIMILARITY:
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. Chem. 276:31502-31509(2001).
                                                             TISSUE SPECIFICITY: Found in cartilage DOMAIN: THE SPACER DOMAIN AND THE TSP TO FOR A TIGHT INTERACTION WITH THE EXTRACE THE PRECURSOR IS CLEAVED BY A FURI
                                                                                                                            matrix (By similarity).
TISSUE SPECIFICITY: Fou
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DISINTEGRIN-LIKE
                    PEPTIDASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Engle J.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B9D2CE023266FC27 CRC64;
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                                               EXTRACELUCIAR MATRIX.

A FURIN ENDOPROMITA
                      FAMILY
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DOMAIN
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human
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SIMILARITY: CONTAINS 4 TSP TYPE-1 DOMAINS. CAUTION: HAS SOMETIMES BEEN REFERRED TO ADAMTS4.

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1051 SKRSST-LPP--PYLLEAAETHDDVISNPSDLPRSLVMPTSLVP 1091

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CARBOHYD
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PROSITE; PS50092; TSP1; 2.

PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.

PROSITE; PS00427; DISINTECRIN_1; FALSE_NEG.

Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;

Hydrolase; Metalloprotease; Heparin-binding.
                                                                                                                                                                                                                                                                                                                                                             CHAIN
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                           METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF247668; AAK28400.1; EMBL; AB002364; BAA20821.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/
                           991
                                                                                                    876
       162 QPDSSTLLPPRSPIALEATEL -----
                                            131
                                                              931 VRCLQPLLDGTNRSVHSKYCMGDRPESRRPCNRVPCPAQWKTGPWSECSVTCGEGTEVRQ 990
                                                                                  95
                                                                                                                       40
                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration -
                           VLCRAGDHCDGEKPESVRACQLPPCNDEPCLGDKSIFCQMEVLARYCSIPGYNKLCCESC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              605011;
                                                                                  ---MOTLLEDVNTEIHFV----
                                                                                                    SDNKMVHRSFCEANKKPKPIRRMCNIQECTH----PLWVAEEWEHCTKTCGSSGYQLRT 930
                                                                                                                      SNFKVKFRELTDHLLKDYPVTVAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF01562; Pep_M12B_propep;
; SM00209; TSP1; 4.
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                                                                                                                                         l Similarity
49; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : IPR002870;
: IPR001590;
: IPR000884;
: IPR000130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR001762; Disintegrin.
IPR002870; Pep_M12B_propep.
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242
345
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814
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1205
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                                                                                                                                         Conservative
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                                                                                                                                                                              AA;
                                            KDTCTQLLALKPCIGKAC-
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712
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21.9%;
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                                                                                                                                                                              135570
                                                                                                                                       22;
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W
                                                                                  ----TSCTFQPLP---
                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
ZINC (CATALYTI
ZINC (CATALYTI
                                                                                                                                                                                                                  N-LINKED
N-LINKED
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TSP TYPE-1
TSP TYPE-1
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                                                                                                                                                  Pred.
                                                                                                                                                           Score 84.5;
                                                                                                                                                                                       N-LINKED
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                                                                                                                                                                                                                                                                                             SPACER
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                                                                                                                                                                                                                                                                                                                                                             ZINC (CATALYTIC)
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                                                                                                                                                                                                                                                                                                               TSP TYPE-1 1.
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                                                                                                                                         Mismatches
-PEPRPRQLLLLLLLP
                                                                                                                                                                              EB07B286FC85FB87 CRC64;
                                                                                                                                                                                                                                                                                                                                  (CATALYTIC)
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(GLCNAC...)
(GLCNAC...)
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                                                                                                                                                          Length 1205;
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SIMILARITY).
        198
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                                                                                  ECLREV--QTNISH 130
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RESULT 7
AEX3_CAEEL
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                                                                             Matches
                                                                                         Best
                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                               Pfam; PF02141; DENN; 1. Pfam; PF03455; dDENN; 1. Pfam; PF03456; uDENN; 1.
                                                                                                                                                                                                                                    InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (Son send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Bristol N2;
MEDLINE-97282461;
                                                                                                                                              DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                           EMBL; U93842; AAB52421.1; EMBL; U49945; AAC47926.1;
                                                                                                                                                                                                                                                                                                                                         modified and this statement
                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in synaptic transmission.";
EMBO J. 19:4806-4816(2000).
-i- FUNCTION: GUANINE NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERACTION WITH CAB-1.
MEDLINE=20428446; PubMed=10970871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leimbac D., Minx M.;
Submitted (FEB-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Iwasaki K., Staunton J., Saifee O.,
"aex-3 encodes a novel regulator of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=6239;
                                                                                                                                SEQUENCE
                                                                                                                                                                     Guanine-nucleotide releasing
                                                                                                                                                                                                                                                                WormPep; C02H7.3;
                                                                                                                                                                                                                                                                                                                                                                                                                        -!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF NEURONS -!- SIMILARITY: CONTAINS 1 DENN DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Iwasaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neuron 18:613-622(1997).
                                                                                                                                                                                                                         InterPro;
                           317
 63
                                                                                         Local
                                                   4 LAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFREL-TDHLLKDYPVTVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGULATE TWO DIFFERENT PATHWAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aki K., Toyonaga R.;
rab3 GDP/GTP exchange factor homolog
VNLQDEKHCKALWSLFL---
                        LLPAYMPSAE - - QLLLAPTPFLIGVPSSFFHHR - -
                                                                             54;
                                                                                         Similarity
                                                                                                                                                                                                                        IPR005113; uDENN
                                                                                                                                                                                                                                    IPR001194; DENN. IPR005112; dDENN
                                                                                                                                1409 AA;
                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   BINDS TO CAB-1
                                                                                                                                                                                                                                                                          AAB52421.1; -. AAC47926.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=9136770;
                                                                                                                                                                                                                                                               CE16806.
                                                                                                                                              632
                                                                                                                                                          364
                                                                                                                                                                                                                                                                                                                                                        institutions as long as its content
                                                                                         6.9%;
23.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to the EMBL/GenBank/DDBJ databases
                                                                                                                                157458 MW;
                                                                          31;
                                                                                                                                                                                                                                                                                                                               agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                            is not removed.
                                                                                         Score 84;
Pred. No.
 -AQRWIEQLKTVAGSKMQTLLEDVNTE---
                                                                                                                                              SER-RICH
                                                                                                                                                          DENN
                                                                                                                                                                      factor.
                                                                             Mismatches
                                                                                                                                2DDE6395AC963313 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FOR NEURAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nonet M., Thomas J.H. presynaptic activity
                                                                                                      DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEX-3 has a dual function
                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                            Usage
                                                                             73;
                           KIRELPSDVILVDLD-TNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTIVITIES
                                                                                                       Length 1409;
                                                                              Indels
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                                                                               68;
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                                                                             Gaps
                           365
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    105
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RESULT 8

CRSP1_MOSE

ID CSSP1_MA

AC P07141

DT 01-FEB

REDLIN

REDLIN

RA DELIN

RA MEGIOUE

RA MEGIOUE

RA MEGIOUE

RA MEGIOUE

RA MEGIOUE

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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES-Mouse;
MEDLINE-87147232; PubMed-3493488;
Parawashisth T.B., Eng R., Shadduck R.K., Waheed A.,
                                                                                          CSF-1 gene.
                                                                                                                                                                                                                                                                                                                      Ben-Avram C.M., Shively J.E., Rajavashisth T.B., Lusis A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=88320507; PubMed=2457916;
Ladner M.B., Martin G.A., Noble J.A., Wittman V.P., Warren M.K.,
McGrogan M., Stanley E.R.;
"cDNA cloning and expression of murine macrophage colony-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=87174763; PubMed=3494232; Delamarter J.F., Hession C., Semo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Macrophage colony stimulating factor-1 precursor
CSF1 OR CSFM.
Mus musculus (Mouse), and
                                               Biochim.
                                                                differentiation.",
                                                                                                                                    Borycki A.G., Lenormund J.,
                                                                                                                                                          MEDLINE=93363632; PubMed=8357831;
                                                                                                                                                                                         SPECIES=Rat;
                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=85242709; PubMed=3925458;
                                                                                                                                                                                                                                                                                                                                                                                             SPECIES-Mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 33-57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning and tissue-specific expression of stimulating factor mRNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 15:2389-2390(1987)
                                                                                                             Isolation and characterization of
                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-100 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Nucleotide sequence of a cDNA encoding (Macrophage-CSF).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mermod
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01-FEB-1996 (Rel. 33, Last seq
30-MAY-2000 (Rel. 39, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSF1_MOUSE
P07141;
                                                                                                                                                                                                                                                                                               Amino-terminal amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090, 10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  476
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    OF.
                                          Biophys.
                                                                                     Post-transcriptional
                                                                                                                                                                                                                                                      Acad.
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                                                                                                                                                                                 STRAIN=Wistar;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -IHFVTSC
                                        Acta 1174:143-152(1993)
                                                                                                                                                                                                                                                      Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sci. U.S.A. 84:1157-1161(1987).
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                                                                                                                                                                                                                                                    U.S.A.
                                                                                                                                                                                                                                                                                            sequence of murine colony-stimulating
                                                                                                     Guillier M., Leibovitch S.A.; tion of a cDNA clone encoding for rat
                                                                                                                                                                               TISSUE=Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Semon
                                                                                                                                                                                                                                                    82:4486-4489(1985)
                                                                                                                                                                                                                                                                                                                                            Shadduck R.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85:6706-6710(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                   repression occurs in myogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TFQPLPECLRFVQTNISHLLKDTCTQLLALK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mouse
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CARBOHYD
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VARIANT
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning and characterization of the murine promoter stimulating factor-1-encoding gene."; Gene 102:165-170(1991).
                                                                                                                                  119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
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      189
                                                                                        129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Harrington M.A., Edenberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91340149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=Mouse;
                                                                                                                                                                            76
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                                                                                                                                                                                                                                                                18
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                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION, DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: THIS CSF INDUCES MACROPHAGES.
SUBUNIT: HOMODIMER, LINKED BY THREE DISULFIDE BONDS.
CNCLYPKATPSSDFASASPHQPPAP----SMAPLA----
                                       SSTLLPPRSPIALEATELPEPRPRQLLLLLLLLPLTLVLLAAAWGLRWQRARR 217
                                                                                                                                                                      DDPVCYLKKAFFLVQDIIDETMRFKDNTPNANATERLQELSNNLN-----
                                                                                                                                                                                                                                                                                                  SSLLLLLLLLSPC1RGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVTVAVNLQDEKH-
                                                                                 EQNKACVRTFHETPLQLLEKIKNFFNETKNLLEKDWNIFTKNCNNSFAKCSSRDVVTKPD
                                                                                                                                                                                                                                                          SRLLEVCLLMSRSTAKEVSEHCSHMIGNGHLKV-LQQLIDSQM-ETSCQIAFEFVDQEQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGI:1339753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A31401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A26575; A26575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A23166;
                                                                                                                                                                                                                                                                                                                                                L Similarity
54; Conser
                                                                                                                                                                                                                  -CKALWSLFLAQRWIEQL--
                                                                                                                              -CLR-FVQT-----NISHLLKDTCTQLLALKPCIGKACQN-FSRC--LEVQCQPD 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                    246
552 AA;
                                                                                                                                                                                                                                                                                                                                                Conservative
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Edenberg H.J., Saxman S.M., Pedigo L.M., Daub R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                license agreement
                                                                                                                                                                                                                                                                                                                                                                6.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                    MW.
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                                                                                                                                                                                                                                                                                                                                                36;
                                                                                                                                                                                                                                                                                                                                                                                                                            MISSING (IN REF. 3).
A -> R (IN REF. 3).
AG -> PR (IN REF. 3).
P -> A (IN REF. 1).
W; 3886D7ZD70E770AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D -> G.
                                                                                                                                                                                                                                                                                                                                              Pred. No. 6.2;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  Score 83.5;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . . ) (POT
N-LINKED (GLCNAC. . . ) (POT
N-LINKED (GLCNAC. . . ) (POT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MACROPHAGE COLONY STIMULATING FACTOR-1.
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                              ---KTVAGSKMQTLLEDVNTEIHFVTSCTFQPLP 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                              94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Usage
-GLAWDDSQR 228
                                                                                                                                                                                                                                                                                                                                                                                      Length 552;
                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) (POTENTIAL).
) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for
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                                                                                                                                                                      SCFTKDYE
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                                                                                                                                                                                                                                                                                                                                            49;
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RESULT 9
ZAN_PIG
  factor.";
J. Biol.
-!- FUNCT
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Q28983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBUNT: PROBABLY FORMS COVALENT OLIGOMERS.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON THE APICAL REGION OF THE SPERM HEAD (BY SIMILARITY).
-!- TISSUE SPECIFICITY: IN TESTIS, PRIMARILY IN HAPLOID SPERMATIDS.
NOT IN LUNG, LIVER, HEART, SPLEEN, BRAIN, KIDNEY, EPIDLDYMIS.
-!- DOMAIN: THE MAM DOMAINS PROBABLY MEDIATE SPERM ADHESION TO THE ZONA PELLUCIDA.
-!- DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS,
-!- DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS,
-!- POMAIN: THE DOMAIN MIGRATION TO THE OVIDUCTAL ISTHMUS.
-!- DOMAIN: THE WORD DOMAINS 2 AND 3 MAY MEDIATE COVALENT
OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUC2).
-!- PTM: THE MAM DOMAINS AND THE MUCIN-LIKE DOMAINS ARE MISSING
FROM THE ZONADHESIN THAT BINDS TO THE EGG EXTRACELLULAR MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             920-925; 96
1658-1667;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zonadhesin
                                                                                                                            Pfam;
                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the egg extracellular matrix is homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Meishan; TISSUE-Testis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
15-JUN-2002 (Rel.
                                                                                     Pfam;
                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                           between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hardy D.M., Garbers D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96064658; PubMed=7592795;
                                                                                                                                            InterPro
                                                                                                                                                        InterPro;
                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A sperm membrane protein that binds in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              scrofa
                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: CONTAINS 2 MAM DOMAINS. SIMILARITY: CONTAINS 4.5 VWFD DOMAINS. SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                             CAPACITATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                          PROCESSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNALING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: BINDS
                              ; PP00094; vwd; 4.
; PP00059; MAM; 2.
; PP01826; TIL; 5.
; PP01826; TIL; 5.
; PF02345; TILa; 5.
; SM00181; EGF; 1
T; SM00137; MAM; 2
T; SM00216; VWD; 4.
                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                            U40024; AAC48486.1; -. P56682; ICCV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. Chem. 270:26025-26028(1995).
NCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA
THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION AND/OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A., AND SEQUENCE OF 823-830; 859-872; 883-890; 960-967; 1235-1244; 1349-1354; 1518-1532; 1624-1656; 7; 1777-1795 AND 1914-1921.
                                                                                                                                           IPR003328;
IPR001007;
IPR001846;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eutheria; Cetartiodactyla;
                                                                                                                                                                                    IPR002919;
                                                                                                                                                                                                   IPR000561;
IPR000998;
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EGF_1;
EGF_2;
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                                                                                                                                                                                                                                                                                   license agreement (See http://www.isb-sib.ch/announce/
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TILa_Cysrich.
VWF_C.
                                                                                                                                            VWF_D.
                                                                                                                                                                                                   MAM_domain.
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actyla; Suina; Suidae;
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                                                         O1-JAN-1990 (Rel. 13, Created)
O1-JAN-1990 (Rel. 13, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Leukosialin precursor (Leucocyte sialoglycoprotein)
(CD43) (W3/13 antigen) (Fragment).
SPN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUB-Thymocytes;
MEDLINE-8816646; PubMed-2965006;
Killeen N., Barclay A.N., Willis A.C., Williams A.F.;
"The sequence of rat leukosialin (W3/13 antigen) reveals a molecule "The olinked glycosylation of one third of its extracellular amino".
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Type I membrane protein. TISSUE SPECIFICITY: CELL SURFACE OF THYMOCYTES, NEUTROPHILS, PLASMA CELLS AND MYELOMAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTM: HAS A HIGH CONTENT OF STALTC ACID AND O-LINKED CARBOHYDRATE STRUCTURES.
     APASSIPL --
                                SPNSSLLLLLLLSPCLRGTPDC---YFSHSPISSNFKVKFRELT----
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                                                                                          Similarity
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GTPELSSFFFTSAGASGNTPVP--ELTTSQEVSTEASLVLFP 106
                                                                                                                                             ME.
                                                                        24;
                                                                                                                                                                                        O-LINKED
                                                                                                                                                        O-LINKED
                                                                      Pred. No. 4.9
; Mismatches
                                                                                     Score 82.5;
Pred. No. 4
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CYTOPLASMIC (POTENTIAL)
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                                                                                                                                         CRC64;
                                                                                                     Length 378;
                                                                    Indels
                                                                                                                                                                                          (POTENTIAL).
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APA4_MOUSE
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                                                                                      COMPONENT OF HOL AND CHYLOMICROS.

C-!- SUBCELLULAR LOCATION: EXTRACELLULAR.

C-!- TISSUE SPECIFICITY: SECRETED IN PLASMA.

C-!- TISSUE SPECIFICITY: SECRETED IN PLASMA.

C-!- DOMAIN: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS (EACH ACTUALLY A TANDEM ARRAY OF TWO, A AND B, RELATED 11-

C-- MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-

C-- MELICAL, AND MANY OF THESE HELICES ARE AMPHIPATHIC. THEY MAY

C-- THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH LECITHIN: CHOLESTEROL

C-- ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.

C-- POLYMORPHISM: THERE IS A POLYMORPHISM WITHIN A SERIES OF IMPERFECT

C-- POLYMORPHISM: THERE IS A POLYMORPHISM WITHIN A SERIES OF IMPERFECT

C-- POLYMORPHISM THERE SEQUENCE E-Q-- (AV)-Q. INSERTIONS OR DELETIONS

C-- POLYMORPHISM SERVE SAVE GIVEN RISE TO THREE FORMS CHARACTERIZED BY

THREE (129), FOUR (C57BL/6), OR FIVE (M.CASTANEUS) COPIES OF THE
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Furnament Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                      Reue K., Leete T.H.;

"Genetic variation in mouse apolipoprotein A-IV due to insertion deletion in a region of tandem repeats.";

J. Biol. Chem. 266:12715-12721(1991).

-!- FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION CATABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN LIPASE BY APOC-II; POTENT ACTIVATION OF LCAT. APOA-IV IS A MAJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APOA4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1988 (Rel.
01-OCT-1996 (Rel.
15-DEC-1998 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J, and 129/J; MEDLINE=91286309; PubMed=16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a high-l
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1988 (Rel. 06, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Apolipoprotein A-IV precursor (Apo-AIV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REVISIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=87089722; PubMed=3796595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
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                                                                       SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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Matches 37
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P28172;
30-MAY-2000
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                                                      P28172;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
Interferon tau precursor (IFN-tau) (Trophoblast protein-1) (TP-1)
Interferon tau precursor (Antiluteolysin) (Trophoblast antiluteolytic protein-1)
                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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REPEAT
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                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae; Ovibos.
                                                  Ovibos moschatus (Muskox)
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NCBI_TaxID=37176;
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                                                                                                                                                                                 262
                                                                                                                                                                                                    116
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                                                                                                                                                                                                                                                                               11 NSSLLLLLLLSPCLR-----GTPDCYFSHSPISSNFKVKF----RELTDHL---LK 55
                                                                                                                                                                                          PLPECLREVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLP 170
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                                                                                                                                                                               QL-----QKNLAPLVEDVQSKVKGNTEGLQKSLEDLNRQLEQQVEEFRRTVEP
                                                                                                                                                                                                                      ELKATIDQNLEDLRRSLAPLTVGVQEKLNHQMEGLA-FQMKKNAEELQTKV----SAKID
                                                                                                                                                                                                                                          DYPVTVAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQ 115
                                                                                                                                                                                                                                                             NTQTQEMKLQLTPYIQRMQTTIKENVDNLHTSMMPLATNLKDKFNRNMEELKGHLTPRAN 206
                                                                                                                                                                                                                                                                                                              Similarity
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21.1%;
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E -> R (ÎN REF. 1).
S -> A (ÎN REF. 1).
RQ -> KA (ÎN REF. 1).
NK -> GG (ÎN REF. 1).
                                                                                                                                                                                                                                                                                                   Score 80.5; I
Pred. No. 7.8;
12; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                          GLU/GLN-RICH
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                                                                                                                                                                                                                                                                                                                       Length 395;
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Query Match
Best Local
                                                                     DISULFID CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THE MONONUCLEAR CELLS OF THE EXTRA-EMBRYONIC TROPHECTODERM.

-!- DEVELOPMENTAL STAGE: MAJOR SECRETORY PRODUCT SYNTHESIZED BY THE CONCEPTUS DURING A VERY SHORT PERIOD IN EARLY PREGNANCY.

-!- MISCELLANEOUS: ITN-TAU GENES ARE INTRONLESS. THEY EVOLVED FROM IFN-OMEGA GENES IN THE RUMINANTIA SUBORDER AND HAVE CONTINUED TO DUPLICATE INDEPENDENTLY IN DIFFERENT LINEAGES OF THE RUMINANTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and
                                                                                                                                                                                                                                                                                                                                                                                                                                     This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "IFN-tau: a novel subtype I IFN1. Structural characteristics, non-ubiquitous expression, structure-function relationships,
                                                    SEQUENCE
                                                                                                                         CHAIN
                                                                                                                                                                                                         ProDom;
                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
use by non-profit institutions as lo
modified and this statement is not remo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: SECRETED INTO THE UTERINE LUMEN
-!- TISSUE SPECIFICITY: CONSTITUTIVELY AND EXCLUSIVELY EX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   potentialities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Guillomot M.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Martal J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=92242937; PubMed=1374107;
                                                                                                       DISULFID
                                                                                                                                          SIGNAL
                                                                                                                                                                                                                             PRINTS; PR00266;
                                                                                                                                                                                                                                              Pfam; PF00143; interferon;
                                                                                                                                                                                                                                                          HSSP; P01563; 2HIE.
InterPro; IPR000471; Interferon_abd
                                                                                                                                                                                                                                                                                                                                                                                                                     between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pregnancy hormonal embryonic signal and cross-species therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99081096; PubMed=9865498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leaman D.W., Roberts R.M.; "Genes for the trophoblast interferons in sheep,"
                                                                                                                                                        Pregnancy;
                                                                                                                                                                            PROSITE; PS00252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REVIEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d distribution of related genes among mammals. Interferon Res. 12:1-11(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RECEPTOR EXPRESSION IN THE ENDOMETRIUM. THIS RESULTS IN THE SUPPRESSION OF THE DUISATILE ENDOMETRIAL RELEASE OF THE LUTEOLYTIC HORMONE PROSTAGLANDIN F2-ALPHA, HINDERING THE REGRESSION OF THE CORPUS LUTEOM (LUTEOLYSIS) AND THEREFORE A RETURN TO OVARIAN CYCLICITY. THIS, AND A POSSIBLE DIRECT EFFECT OF IFN-TAU ON PROSTAGLANDIN SYNTHESIS, LEADS IN TURN TO CONTINUED OVARIAN PROGESTERONE SECRETION, WICH STLMULATES THE SECRETION BY THE ENDOMETRIUM OF THE NUTRIENTS REQUIRED FOR THE GROWTH OF THE CONCEPTUS. IN SUMMARY, DISPLAYS PARTICULARLY HIGH ANTIVIRAL AND ANTIPROLIFERATIVE POTENCY CONCURRENTLY WITH PARTICULAR WEAK CYTOTOXICITY, HIGH ANTILUTEOLYTIC ACTIVITY AND IMMUNOMOBULATORY PROPERTIES. IN CONTRAST WITH OTHER IFNS, IFN-TAU IS NOT VIRALLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THEY ENCODE FOR PROTEINS VERY SIMILAR IN SEQUENCE BUT WITH DIFFERENT BIOLOGICAL POTENCY AND PATTERN OF EXPRESSION. SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: PARACRINE HORMONE PRIMARLY RESPONSIBLE FOR MATERNAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RECOGNITION OF PREGNANCY. I PROBABLY TYPE I INTERFERON EXPRESSION, PREVENTING THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FAMILY. IFN-ALPHAII SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                               M73244; AAA31583.1; -.
                                                                                                                                                                                           SM00076;
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101
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                                                    AA;
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195
122
162
101
22370 1
                                                                                                                                                                                           IFabd;
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                                                                                                                                                                        INTERFERON_A_B_D; 1
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6.5%;
27.4%;
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BY SIMILARITY.
INTERFERON TAU.
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                Score
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                DB 1;
                                                                                                                                                      Signal;
              Length 195;
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                                                      CRC64;
                                                                                                                                                    Glycoprotein
                                                                   (POTENTIAL)
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Matches

34; Conser

Conservative

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Mismatches No.

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RA Wood V. Gwilliam R., Haylandream M.A., Lyne M., Lyne R., Stewart A.,
RA Boouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Gulter S., Suunders D., Seeger K., Sharp S.,
RA William K., Fritzc C., Folzares R., Squares S., Stevens K.,
RA Weltjens I., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moree K., Hurst S.M.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe S., Janenez J., Sanchez M., del Rey F., Benito J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Cerrutti L., Lowe G., Darrell B.G., Nurse P.;
RT The genome sequence of Schizosaccharomyces pombe.";
RT Nature 415:871-80(2002).
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                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Hypothetical protein C31A2.16 in chromosome
SPAC31A2.16.
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                                                                                 EMBL; Z50113; CAA90474.1; -
                                                                                                                                                                 modified and this statement is not removed.
                                                                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long
                                                                                                                                                                                                                                                                                             -!- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY (DH) DOMAIN.
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Q09733;
                                     InterPro; IPR001331; GDS_CDC
InterPro; IPR000219; RhoGEF.
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Best Local Similarity
                                                                                                                                                                                                                                                                               Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C., III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
                                                                        Submitted (APR-2001) to the EMBL/GenBank/DDF-i- SUBCELLULAR LOCATION: Integral membrane-i- SIMILARITY: TO E.COLI YIDH.
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                    Fleischmann R.D., Alland D., Eisen J.A., Carpenter I., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.I., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg, Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium NCBI_TaxID=1773;
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                                                                                                                                                          Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein Rv2272. Rv2272 OR MT2333 OR MTCY339.38C.
                                                                                                                        "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98295987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis
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RESULT 15
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Best Local
                                                                                                                                                              Genomics 61:268-276(1999).

1. SUBCELLULAR LOCATION: Nuclear (Potential).

1. DISEASE: DEFECTS IN RECQL4 ARE A CAUSE OF ROTHMUND-THOMSON

SYNDROME (RTS). A DISEASE CHARACTERIZED BY DERMAROLOGICAL FEATURES

SUCH AS ATROPHY, PIGMENTATION, AND TELANGIECTASIA AND FREQUENTLY

ACCOMPANIED BY JUVENILE CATARACT, SADDLE NOSE, CONGENITAL BONE
                                                                                                                                                                                                                                                                                                                                                MEDLINE-99097344; pubMed-9878247;
Kitao S., Ohsugi I., Ichikawa K., Goto M., Furuichi Y., Shimamoto A.;
"Cloning of two new human helicase genes of the RecQ family:
biological significance of multiple species in higher eukaryotes.";
Genomics 54:443-452(1998).
                                                                              This
                                                                                                                                                                                                                                                                       MEDLINE=20021764; PubMed=10552928;
Kitao S., Lindor N.M., Shiratori M., Fu
"Rothmund-Thomson syndrome responsible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ATP-dependent DNA helicase Q4 (RecQ protein-like
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                                             European Bioinformatics Institute.
                                                                                                  DEFECTS, DISTURBANCES OF HAIR GROWTH, AND HYPOGONADISM.
SIMILARITY: BELONGS TO THE HELICASE FAMILY. RECQ SUBFAMILY.
DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
WWW-"http://www.infobiogen.fr/services/chromcancer/Genes/RECQL4ID285.html"
                                                        SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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PF02656; DUF202; 1.

Metical protein; Transmembrane; Complete proteome.

MEM 33 53 POTENTIAL.

MEM 58 78 POTENTIAL.

MEM 97 117 POTENTIAL.

MEM 97 117 POTENTIAL.

MEM 97 117 POTENTIAL.
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29; Conservative
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 non-profit institutions as long and this statement is not removed requires a license agreement (See
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Pfam; PF00271; helicase_C; 1.
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EMBL; AB026546;
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                      ELPEPRPRQLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPS
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SM00490; HELICC; 1.
SM00343; ZnF_C2HC; 1.
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Q9Н9U7	Q9LS68	Q9XET3	Q9DBY4	Q9SN38	Q9T7T9	Q9ZY32	Q85034	Q85032	Q9VNP5	Q8T0N4	Q9W2D7	Q9UMT2	Q9B6D1	Q9N4U7	Q9KQC8	Q96AY5	Q9MBF8	006521	017726	096164	Q9GPN8	Q91802	Q9VF50	Q8ZH99	Q9FKE2	Q9CYB2	Q9VF51	Q8SXA6
ⅎ	<u>.</u> .	Q9xet3 lycopersico	Q9dby4 mus musculu	arabid		Q9zy32 orycteropus		2	-	Q8t0n4 drosophila	Q9w2d7 drosophila	Q9umt2 homo sapien	Q9b6d1 yarrowia li	Q9n4u7 caenorhabdi	8	_	Q9mbf8 chlamydomon			096164 plasmodium			drosophila	Ψ	Q9fke2 arabidopsis	$\sim$	Q9vf51 drosophila	Q8sxa6 drosophila

### ALIGNMENTS

PRELIMINARY;

PRT;

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RESULT 1
Q61104
ID Q611
AC Q611
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                                                                                                                                             Query Match
Best Local S
Matches 165
                                                                                                                                                                                                                                                                                                                                                                                                        Q61104
Q61104;
01-NOV-1996 (
01-NOV-1996 (
01-JUN-2002 (
Flt3 ligand,
                                                                                                                                        forms and processing.";
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U44024; AAA93305.1; -.
MGD; MGI:95560; Flt31.
InterPro; IPR004213; Flt3_lig.
InterPro; IPR001230; Prenyl_site.
InterPro; IPR001230; Prenyl_site.
Pfam; PF02947; flt3_lig.
PROSITE: PS00294; PRENYLATION; UNKNOWN_1.
SEQUENCE 172 AA; 19465 MW; 04F0A010171E3384 CRC64;
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MCClanahan T., Culpepper J., Campbell D., Wagner J., Franz-Bacon K.,

Matteson J., Tsai S., Luh J., Guimares M.J., Mattei M.-G., Rosnet O.,

Birnbaum D., Hannum C.;

"Flt3 ligand: expression, genomic organization, alternatively spliced
                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                  FLT3L
             61
                                      VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
165;
                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          i (TrEMBLrel. (5 (TrEMBLrel. (2 (TrEMBLrel. ; 2 ), T169 form.
                                                                                           Conservative
                                                                                                      71.9%;
98.2%;
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01,
21,
                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                        Score 879; DB 11;
Pred. No. 1.5e-81;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172
                                                                                                                   Length 172;
                                                                                          Indels
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                                                                                          Gaps
               120
                                         60
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Q8VCH
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                         MEDLINE=20570936; PubMed=11120823;
Mwangi W., Brown W.C., Palmer G.H.;
"Identification of fetal liver tyrosine ki
required for receptor binding and function
ligand isoforms.";
J. Immunol. 165:6966-6974(2000).
EMBL; AF282985; AAF99322.1;
InterPro; IPR004213; Flt3_lig.
Prom; PF02947; flt3_lig; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.; submitted (DEC-2001) to the EMBL/GenBank/DDBJ EMBL; BC019801; AARI19801.1; -. InterPro; IPR004213; Flt3_lig. Pfam; PF02947; flt3_lig; 1.
                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9GKE0;
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
        SEQUENCE
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. Flt3 ligand isoform-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9GKE0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence upd
01-JUN-2002 (TrEMBLrel. 21, Last annotation u
Similar to FMS-like tyrosine kinase 3 ligand.
                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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     ĀΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18986 MW;
  32390 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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Pred. No. 7.7e-78;
0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
     D68B9ED79221202D CRC64;
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                                                                                                                                                                 function
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using
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                                                                                                                                                                                       ligand
                                                                                                                                                                                                                                                                                                                                                                               Bovoidea;
                                                                                                                                                              occurring
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Q8WNW1
ID .08WN
AC Q8WN
DT 01-M
DT 01-M
DT 01-J
DE F1t3
GN F1t3
GN F1t3
GN F1t3
GN F1t3
CC Buka
OC Mamm
OC Bovi
RN [1]
RP SEQUE
RA Hikc
RT "Clc
RT Subm
DR Ffan
DR Pfan
SQ SEQUE
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Best Local
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239
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Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Flt3 ligand.
FLT3 LIGAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 01-MAR-2002 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning of a cDNA for bovine flt3 ligand.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8WNW1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8WNW1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                      1 MTVLAPAWSPNSSLLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
                                                                                                                                                                                                   DTESELGGSQLEPG-PFLGHP
                                 -----GELHPGVPLPSHP
                                                                SLPGPQSPLLLLLLLLLPVALLLLATAWCLCRWRRRRTRYPGERRRTLRPRESSHLPA
                                                                                                 ELPEPR-PRQLLLLLLLLPLTLVLLAAAWGL-RWQRARRR---
                                                                                                                                  LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
                                                                                                                                                                                                                                                                     MVVLAPAWSPTTSLLLLLLLLSPGLQGTPDCSFRHSPISSTFAIKIGKLSKYLLQDYPVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MTVLAPAWSPNSSILLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DTESELGGSQLEPG-PFLGHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRFVQANISHLLQDTHQQLEALKPWI--THRNFSRCLELQCQPDSPTLLPPRSPGALGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VASNLQDDKLCGAFWRLVLAQRWMGRLKTVAGSEMEKLLEDVNTEIHFVTSCAFQPLPSC
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                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                         292 AA;
                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                       32388 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.7%;
63.2%;
                                                                                                                                                                                                                                                                                                                                                       63.3%;
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21,
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.2e-70
); Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                      Score 774.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 779.5; DB 6 Pred. No. 3.7e-71;
                                                                                                                                                                                                                                                                                                                                                                                                       2A797E0C1199C1D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AΑ
                                                                                                                                                                                                                                                                                                                                                                      DB 6;
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                                                                                                                                                                                                                                                                                                                                       44;
                                                                                                                                                                                                                                                                                                                                                                     Length
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                                                                                                                                                                                                                                                                                                                                                                        292;
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                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                 218
                                                                                                                                                                   180
                                                                                                                                                                                                                                    120
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RESULT
Q9MZU9
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Query Match
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000
01-OCT-2000
01-JUN-2002
                                                                 Yang S., Sim G.K.;
"Molecular cloning of canine and feline flt3 ligand reveals high degree of similarity to the human and mouse homologue but unique long cytoplasmic domain.";
DNA Seq. 11:163-166(2000).
                                                                                                                                                                    Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
                                                                                                                                                                                                            01-JUN-2002
Flt3 ligand
                                                                                                                                                                                                                                                                  Q9MZU9
                     SEQUENCE
                                   Pfam; PF02947;
                                                                                                                                                                                                                                                       Q9MZU9;
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                                                        EMBL;
                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=20358731; PubMed=10902925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; ve
Mammalia; Eutheria; Carnivora; Fissipedia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   degree of similarity to the human
long cytoplasmic domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=20358731; PubMed=10902925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9MZV0;
                                            InterPro;
                                                                                                                                                             NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Seq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecular cloning of canine and feline flt3 ligand reveals high
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, AF155148; AAF87088.1; -.
xrPro; IPR004213; F1t5_11g.
1; PF02947; f1t3_11g; 1.
JENCE 294 AA; 32394 MW; (
                                                                                                                                                                                                                                                                                                                          LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MTVLAPAWSPNSSLLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S., Sim G.K.;
                                                                                                                                                                                                                                                                                                                                               ELPEPR-PRQLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPG 224
                                                                                                                                                                                                                                                                                                                                                                    VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
                                                                                                                                                                                                                                                                                                                                                                                                                   VASNLQDDELCGAFWRLVLAQRWMVRLQAVAGSQMQILLEAVNTEIHFVTFCAFQPLPSC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIVLAPAWSPTAS-LLLLLLLSPGLRGTPDCSFSHSPISSTFAVTIRKLSDYLLQDYPVT 59
                              AF155149; AAF87089.1; -. Pro; IPR004213; Flt3_lig. PF02947; flt3_lig; 1.
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                                                                                                                                                                                                                    (TrEMBLrel.) (TrEMBLrel.)
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                      ΑA;
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Carnivora; Fissipedia; Canidae;
                      32459 MW;
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70.2%;
62.2%;
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21,
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15,
21,
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 774; DB 6;
Pred. No. 1.3e-70;
3; Mismatches 38
Score
                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6859917A3B74ABCD CRC64;
                     8F85A10A5EA0DCC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse homologue but uniquely
761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         294
                                                                                                                                                                                                                                                                 291 AA
                                                                                        mouse homologue but uniquely
DВ
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 294;
                                                                                                                                                                         Felis
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                                                                                                                                                                                  Euteleostomi;
291;
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RESULT
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Best Local :
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J. Immunol. 165:0500

EMBL; AF282986; AAF99323.1; -.

InterPro; IPR004213; Flt3_lig.

Pfam; PF02947; flt3_lig; I

SEOUENCE 274 AA; 30372 MW; 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O9GKD9;
O1-MAR-2001 (TrEMBLrel. O1-MAR-2001 (TrEMBLrel. O1-DEC-2001 (TrEMBLrel. Flt3 ligand isoform-2.
                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20570936; PubMed-11120823; Mwangi W., Brown W.C., Palmer G.H.; Wrosine "Identification of fetal liver tyrosine required for receptor binding and functifigand isoforms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Butheria; Cetartiodactyla; Rur
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9GKD9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                             221
                                                                  219
                                                                                         161
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mes 150; Conserv
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                                                                                                                                                                                                                             1 MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
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                                                                                       LREVQTNISHLLKDTCTQLLALKPCIGKACQNESRCLEVQCQPDSSTLLPPRSPIALEAT
                                                                                                                                                  LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELPEPRPRQLLLLLLLLPLTLVLLAAAWGLRWQRARRR 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                            DTESELGGSQLEPG-PFLGHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALPAPQ-APLILLLLLLPVALLLMSAAWCLHWRRRRWR 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LREVQTNISHLLQDTSEQLAALKPWITR--RNESGCLELQCQPDSSTPLPPRSPRALEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VASNLQDDELCGPFWHLVLAQRWMGRLKAVAGSQMQSLLEAVNTEIHFVTLCAFQPLPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIVLAPAWSPTTS-LLLLLLLSPGLRGSPDCSFSHSPISSTFKVTIRKLSDYLLQDYPVT
                                                                                                                                                                                                                                                                                                                                                                  165:6966-6974(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                           Conservative
                                                                 -GELHPGVPLPSHP 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                    -DTHQQLEALKPWI - -THRNFSRCLELQCQPDSPTLLPPRSPGALGAT
                                                                                                                                                                                                                                                                          55.5%; Score 678.5; DB 6 57.5%; Pred. No. 6.4e-61; tive 19; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16,
19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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2; Mismatches
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                                                                                                                                                                                                                                                                                                                      725A7F77A95DA98B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.8e-69;
ches 37;
                                                                                                                                                                                                                                                                                                                                                                                        kinase 3
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-94377978; pubMed-8091210;
Bent A.F., Kunkel B.N., Dahlbeck D., Brown K.L.
Giraudat J., Leung J., Staskawicz B.J.;
"RPS2 of Arabidopsis thaliana: a leucine-rich
disease resistance genes.";
Science 265:1856-1860(1994).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
RPS2 (Disease resistance protein RPS2).
RPS2 OR F20B18.200 OR AT4G26090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bevan M., Rose M., Hempel S
Mayer K.F.X., Schueller C.;
Submitted (MAR-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta
Spermatophyta; Magnoliophyta; eudicotyledons; core
eurosids II; Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q42484
Q42484;
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Rose M., Hempel S., Submitted (MAR-2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000767; InterPro; IPR001611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EU Arabidopsis sequencing Submitted (MAR-2000) to the
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ELGFADLEYLENLTTLGITVLSLETLKTLFEFGALHKHIQHLHVEECNELLYFNLPSLTN
                                                                                                VLPQELGNLRKLKHLDLQRTQFLQTIPRDAICWLSKLEVLNLYYSYAGWELQSFGEDEAE
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S; PR00364; DISEASEPO
VCE 000
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U12860; AAA50236.1;
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55; Conserv
                                                                                                                                              VNLQDEKHCKALWSLFL-----AQRWIEQLKTV-----
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A; 104640 MW;
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22.8%;
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Pred. No. 0.52;
40; Mismatches
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                                                                                     Macaca fascicularis (Crab eating macaque) (Cynomolgy Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Cercopithe Cercopithecinae; Macaca.
NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.:
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AKOG6226; BAB15400.1;
SEQUENCE 355 AA; 37894 MW; 52C41A73E673623C CRC64;
Suzuki Y., Sugano S., Hashimoto 
"Isolation of full-length cDNA c 
libraries.";
                                  TISSUE-FRONTAL LOBE LEFT;
Osada N., Hida M., Kusuda J., Tanuma
                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Cr
01-JUN-2001 (TrEMBLrel. 17, La
01-JUN-2002 (TrEMBLrel. 21, La
01-JUN-2002 (TrEMBLrel. 21, La
Hypothetical 56.5 kDa protein
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01-MAR-2001 (TYEMBLIEL 16, Last sequence up
01-DEC-2001 (TYEMBLIEL 19, Last annotation
CDNA: FLJ22573 fis, clone HSI02387.
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                                                              SEQUENCE FROM N.A
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ertebrata; Euteleostomi;
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Best Local
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence resistance protein RPS2
01-JUN-2001 (TrEMBLrel. 17, Last sequence protein update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEM
                                                           Pfam; PF00560; LRR; 4.
Pfam; PF00951; NB-ARC; 1.
PRINTS; PR00364; DISEASERSIST
SMART; SM00382; AAA; 1.
SMART; SM00370; LRR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001611; LRR.
InterPro; IPR000483; LRR_Cterm.
InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
pfam; PF00560; LRR; 6.
Pfam; PF01463; LRRCT; 1.
                                                                                                                                                                                                                                                                  InterPro; IPR003593; AAA_ATPAse.
InterPro; IPR000767; Disease_resist.
InterPro; IPR001611; LRR.
InterPro; IPR003592; LRR_out.
                                                                                                                                                                                                                                                                                                                                                                                                               between RPS2 and other host factors disease resistance.";
Genetics 158:439-450(2001).
EMBL; AF368301; AAK38117.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-21231631; PubMed-11333251;
Banerjee D., Zhang X., Bent A.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein SEQUENCE 510 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS: PR00019; LEURICHRPT. SMART; SM00370; LRR; 4. SMART; SM00369; LRR_TYP; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9ASP5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted
                                    ATP-binding
                                                                                                                                                                                                                                                InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKLHSLQVLVLSNNALRTLRGSWFRNTRGLTRLQLDGNQITNLTDSSFGGTNLHSLRHLD 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSNNFISYIGKDAFRPLPQ-LQEVDLSRNRLAHMPDVFTPLKQLIHLSLDKNQWSCTCDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --LKDYPVTVAVN-----LQDE--KHCKALWSLFLAQRWIEQL--KTVAGSKMQTL--LE 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STNLSLLFNLALLSLSRNGIEDVQEDALDGLTMLRTLLLEHNQISSS-----SLTDHTF 103
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AB055271; BAB21
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68; Conservative
                                                                                                                                                                                                                                         IPR002182; NB-ARC.
       909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
       AA;
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       104613
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       MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 93.5; DB
Pred. No. 0.43;
34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FF52698C2F9119E8 CRC64;
   F83E0F881B409DFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   determine effective interaction in Arabidopsis RPS2-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       909
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RESULT 12
Q83443
ID Q8344
RESULT 13
Q83448
ID 08344
AC 08344
AC 01-N0
DT 01-N0
DT 01-MA
DE VP7.
OS Murin
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Best Local
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                    Q83448
Q83448;
Q1-NOV-1996
Q1-NOV-1996
Q1-MAR-2002
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Q83443;
Q1-NOV-1996
Q1-NOV-1996
Murine rotavirus
                                                                                                                                                                                                                                                                                                                                                                                                                           Murine rotavirus.
Viruses; dsRNA viruses;
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                                                                                                                          EMNDNSWKDTLSQLFLTKGW
                                                                                                                                                NLQDEKHCKALWSLFLAQRW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLPQELGNLRKLKHLDLQRTQFLQTIPRDAICWLSKLEVLNLYYSYAGWGLQSFQEDEVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----VNLQDEKHCKALWSLFL-----AQRWIEQLKTV-----AGSKMQTLLEDVNT
                                                                                                                                                                     LLVILILSPCIKAQNYGINLPITGSMDTAYANSTQSDTF-----LTSTLCLYYPTEAAT
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                    (TrEMBLrel. (TrEMBLrel.)
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(TrEMBLrel.)
(TrEMBLrel.)
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                                                                   PRELIMINARY;
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                                                                                                                                                                                            -GTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVTVAV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation updat
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Pred. No. 1.7;
                    Last sequence update)
Last annotation update)
                                            Created)
                                                                                                                                                                                                                             Score 88.5; DB 12; Pred. No. 0.84;
                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Greenberg H.B.;
"Comparison of VP4 and VP7 of Virology 203:250-259(1994).
EMBL; U08427; AAA50490.1; -.
                                                                                                                                                                                                                              SMART; SM00409; IG; 1
SMART; SM00410; IG_like; 1
SMORT; SM00410; Z8430 MW;
                                                                                                                                                                                                                                                                               InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                           Tracey A.; submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases EMBL; AL136967; CAC09453.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, C
01-MAR-2001 (TrEMBLrel. 19, I
01-DEC-2001 (TrEMBLrel. 19, I
DJ149ML8.1.1 (natural killer
DJ149ML8.1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; dsrNA viruses; Reoviridae; Rotavirus NCBI_TaxID=28327;
                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).

Motazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9Н563;
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                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                      InterPro;
152 NFSRCLEVQCQPDSSTLLP-PRSPIALEATELPEPRPRQLLLLLLLLLPLTLVLLAAAWGL 210
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                                      107
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T; SM0047; Ig. 11;

T; SM0047; Ig. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NLQDEKHCKALWSLFLAQRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLVILILSPCIKAQNYGINLPITGSMDTAYANSTQSETF----
                                    YWCRIYRPSDNSVSKSVRFYLVVSPASASTQTSWTPRDLVSSQTQTQSCVPPTAGARQAP
                                                           --C-TFQP----LPECLRF-----VQTNISHLLKDTCTQLLALKPCI-----GKACQ
                                                                                     -YEKKGWCKEA-SALVCIRLVTSSKPRTMAWTSRFTIWDDPDAGFFTVTMTDLREEDSGH 106
                                                                                                           NLQDEKHCKALWSLFLAQRWIEQLK--TVAGSKMQTLLEDVNTEIHFVTS
                                                                                                                                                          AWSPNSSLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLK---DYPVTVAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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J.W., Cross T.L.,
                                                                                                                                                                            7.2%; 5cc
23.8%; Pre
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Last annotation update)
r cell p44-related gene 1 (NKp44RG1)).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                  Score 88; DB 4; Length 258 Pred. No. 0.73; 1; Mismatches 105; Indels
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l; Mismatches
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                                                                                                                                     -FPGSQAQSKAQV-LQSVAGQTLTVRCQYPPTGSL
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01-MAY-1999 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
KIAA0716 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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InterPro; IPR000194; ATPASE_a/bcentre.
PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
SEQUENCE 765 AA; 86915 MW; EICCAF0771A9E9F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99087487; PubMed=9872452;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 GTPDCYFSHSPISSNFKVKFRELTDHLLK---DYPVTVAVNLQDEKHCKALW----SLFL
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                                                                                                                     TRVIPRRSPLSYPA
                                                                                                                                                                                                                          PQDMRPLHKKLVDQFFVMKSSLG--IQEFSACMQASPVHFPNGSPRVCRNSAPASVSPDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                    VQSLPGISRWFEVEXREVVEMSPLENAIEVLENKNQQLKTLISQCQTRQMQNINPLTMCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ-----TEQLKTVAGSKMQT---LLEDVNTEIH-FVTSC-----TFQPLPECL 121
                                                                                                                                                                                                                                                                                  QTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQ
                                                                                                                                                                                                                                                                                                                                          NGVIDAAVNGGVSRYQEAFFVKEYILSHPEDGEKIARLRELMLEQAQILEFGLAVHEKFV
                                                                                                                                                                     STLLPPRSPIALEA 179
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November
8 secs
                                                                                                                     474
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20,
                                2002, 10:11:41
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 88; 1
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                           -RFV 124
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                                                                                                                                                                                                                                                                                              165
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                                                                                                                                                                                                                                         460
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

November 24, 2002, 10:02:26; Search time 31.2296 Seconds (without alignments) 985.632 Million cell updates/sec

Perfect score: US-09-448-378-2 1223

Sequence: 1 MTVLAPAWSPNSSLLLLLLLL......WQRARRRGELHPGVPLPSHP 231

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Data

DAT:*	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT	23:	
DAT:*	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.	22:	
. DAT: *		21:	
DAT:*	/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.	20:	
. DAT: *	/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998.	19:	
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.DAT: *	/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994.	15:	
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.DAT: *	/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.	13:	
. DAT: *	/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991	12:	
.DAT:*	/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990	11:	
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.DAT:*		9:	
.DAT:*	/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.D	8:	
T:*	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:	7:	
.DAT:*	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.D	6:	
. DAT: *	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.D	<u>ن</u>	
.DAT:*	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.D.	4:	
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T:*	/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.D	2:	
.DAT:*	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.D	1:	
	_Geneseq_101002:*	A_0	base

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

10	9	8	7	6	5	4	ω	2	ப	Result	
879	879	879	1004	1006	1208.5	1212.5	1223	1223	1223	Score	
71.9	71.9	71.9	82.1	82.3	98.8	99.1	100.0	100.0	100.0	Query Match Length DB	æ
220	220	172	189	288	232	232	231	231	231	ength	
22	22	22	22	22	22	16	22	20	16	:	
AAB20190	AAB20188	AAB20191	AAB20187	AAU02129	AAB20189	AAR66177	AAB20186	AAW67768	AAR67540	ID	
Mouse Flt-3 ligand	Mouse Flt-3 ligand	Mouse Flt-3 ligand	Mouse Flt-3 ligand	Flt-3 ligand (FL)	Mouse Flt-3 ligand	Mouse MoT110/T118	Mouse Flt-3 ligand	Murine flt3-ligand	Mouse flt-3 ligand	Description	

5	44	3	42	41	0	39	38	37	36	ω,	34	ω	32	31	30	29	28	27		25							8	17	6	5	14	ω	ถ	
4	541	42.	2	4	4	4	4	48.	73.		63.	66.	S)	67	679.5	œ	œ	8	œ	æ	æ	æ	8	8	9	76	68.	68.	68.	68.	68.		72.	7
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140	101	334	334	523	349	349	349	377	250	178	185	265	276	209	268	209	209	209	209	209	209	209	209	209	212	291	235	235	235	235	235	235	235	294
19	16	19	19	19	19	19	19	19	21	22	22	21	21	21	21	21	21	21	21	21	21	21	19	21	21	21	23	22	21	20	16	22	16	21
AAW77911	AAR66174	AAW77821	AAW83290	AAW78008	AAW78005	(4)	AAW83286	AAW78124	AAY58208	AAB20193	AAB20195	AAY58211	AAY58207	AAY69728	AAY58206	AAY69722	AAY69729	AAY69727	AAY69726	AAY69725	AAY69723	AAY69720	AAW69007	AAY69724	AAY69721	AAY58210	ABB08129	19	AAY69719	76	AAR67541	AAB20194	AAR66175	AAY58204
Human flt3 ligand	gano	SF-F1t-	Human flt3 ligand		139/	n flt3			뜎	ω	u	Feline mature Flt-	ώ	Human flt-3 mutein	Canine mature Flt-	Human flt-3 mutein	Human flt-3 mutein	ယ်	ů	Human flt-3 mutein	flt-3	e wild	f1t-3	ώ	flt-3 n	5	Flt3L p	3 ligan	Full length wild t	Ŀ	Human flt-3 ligand	Human Flt-3 ligand	/S109	Canine Flt-3 ligan

### ALIGNMENTS

RESULT 1
AAR67540
ID AAR67540
XX AAR6
XX AAR6
XX MOUS
XX MOUS
XX MUS
XX MUS
XX MOS
XX 24-MAY-1993; 12-AUG-1993; 25-AUG-1993; Domain Mus sp. Flt-3 ligand; flt3-L; anemia; cancer; AIDS; gene therapy. Mouse flt-3 ligand. 05-AUG-1995 (first entry) AAR67540; AAR67540 standard; Protein; 231 19-MAY-1994; Domain 07-DEC-1994. EP627487-A. Domain Peptide 93US-0068394. 93US-0106463. 93US-0111758. 94EP-0303575 212..231 /label= Cytoplasmic\_domain /label= Extracellular\_domain
189..211
/label= Transmembrane\_domain
212..231 /label= Sig\_peptide 28..188 Location/Qualifiers 1..27 ĀΑ

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RESULT 2
AAW67768
ID AAW6
XX
AC AAW6
XX
DT 25-1
XX
DE Mur
XX
Ant
KW Ant
KW Ant
KW Lim
KW Lim
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OS Mu
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Best Local
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07-MAR-1994;
11-MAY-1994;
           Abbott MM,
                                                        17-JUN-1997;
                                                                             12-JUN-1998;
                                                                                                    23-DEC-1998
                                                                                                                          WO9857655-A1
                                                                                                                                                                 Antigen-specific peripheral immune tolerance; flt3-ligand; flt3-L; immunogenic; autòimmune disease; organ transplantation; food aller tissue transplantation.
                                                                                                                                                                                                                                    25-MAR-1999
                                                                                                                                                                                                                                                                               AAW67768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA encoding mouse flt3-ligand (flt3-L) was isolated from a cDNA library of T-cell line P7B-0.3A4 in CV-1/EBNA-1 cells using a slide autoradiography method. Flt3-L stimulates production of progenitor and stem cells, and can be used e.g.
                                                                                                                                                                                                             Murine flt3-ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 25-27; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beckmann
                         (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
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hes 231;
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                                                                                                                                                                                                                                                                                                                                             ELPEPRPROLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP
                                                                                                                                                                                                                                                                                                                                                                             LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                  VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1995-008071/02.
DB; AAQ79076.
                                                                                                                                                                                                                                                                                                                                    ELPEPRPRQLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                               standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ligands for flt 3 receptors - AIDS and various cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 AA;
           Mowat AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lyman SD;
                                                     97US-0877421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93US-0162407.
94US-0209502.
94US-0243545.
                                                                             98WO-US12085
                                                                                                                                                                                                                                                                               Protein;
            Viney JL;
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Pred. No. 5.2e-115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A method has been developed of initiating or enhancing: (i) an antigen-
Consequence in the project of the mucosal administration of a polypeptide, before, after or with the mucosal administration of an immunotolerising amount of the antigen or therapeutic molecule, respectively. The polypeptide is capable of binding the filt3 receptor and is: a) amino acids 28 x of murine fit3 clipand (fit3-L), where x is an amino acid between 163-231; b) amino acids 28 y of human fit3-L, where y is an amino acid between 160-235; and c) a polypeptide that has at least 90% identity to the polypeptides of either (a) or (b). The method ameliorates the effects of autoimmune diseases, food allergies or organ or tissue rejection following transplantation. Administration of fit3-L allows lower doses of antigens to be used in vivo for mucosally administered antigens. The present of sequence represents murine fit3-L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                    Flt-3 ligand; Fms-like tyrosine kinase; mouse; vaccine;
immunotherapy; therapy; tumour; cancer; melanoma; glioma;
lymphoma; autoimmune disease; infection; gene therapy.
                                                                                                                      Key
Peptide
            Domain
                                                                                                                                                                                                                                              Mouse Flt-3 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 199
N-PSDB;
                                      Domain
                                                                  Domain
                                                                                            Protein
                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                          14-MAY-2001
                                                                                                                                                                                                                                                                                                      AAB20186;
                                                                                                                                                                                                                                                                                                                                AAB20186 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Methods for initiating or enhancing
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DB; AAV81505.
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                                                                                                                                                                                                                                                                          (first
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                                                                                            /label=
28..231
           212.
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28..188
                                        189.
                       /label= Transmembrane_domain
                                                                                                                                    Location/Qualifiers
                                                  /label=
                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                  Extracellular_domain
                                                                                                         Signal_peptide
                                                                            Mature_protein
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Pred. No. 5.2e-115;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 231;
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RESULT 4
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         compositions comprising the polynucleotides are useful for suppressing tumour growth in a mammal. The tumour is melanoma, glioma or lymphoma, particularly B-cell lymphoma. They can also be used for the prophylactic and/or therapeutic treatment of:
(a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis E and C in humans), parasitic (e.g. malaria) and fungal infections;
(b) autolumune diseases (e.g. rheumatoid arthritis and osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polynucleotide may encode the present full-length murine Flt-3 ligand polypeptide, or amino acids 28-163, 1-163, 28-189 or 1-189 of the Flt-3 ligand. The polynucleotides are incorporated into the cells of the vertebrate in vivo, and a prophylactically or therapeutically effective amount of Flt-3 ligand and 1 or more antigens or cytokines is produced in vivo. Pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immune response of a vertebrate to an antigen or a cytokine by administering in vivo, into a tissue of a vertebrate, a FIL-3 ligand-encoding polynucleotide, and I or more antigen- or cytokine-encoding polynucleotides. The FIL-3 ligand-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunogenic compositions comprising Flt-3 ligand encoding polynucleotide and one or more antigen, or cytokine encoding polynucleotides, useful for suppressing transfer growth and for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 120; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autoimmune diseases (e.g. rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (VICA-) VICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             specification.
               AAR66177 standard; Peptide; 232
                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Various
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present sequence
                                                                                                                                                                                                                                                          VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
                                                                                                                                                                                                                                                                                                      MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-123319/13
                                                                                                                                                                                     LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
                                                                                                                                                                                                                                     VAVNLQDEKHCKALMSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                   ELPEPRPRQLLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP 231
                                                                                                                                     ELPEPRPRQLLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP
                                                                                                                                                                     LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ligand)
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                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           other examples of these diseases are given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                             231 AA
                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0146170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The
                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention is directed to enhancing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is that of mouse Fms-like tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                          Score 1223; DB 22; Pred. No. 5.2e-115;
                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arthritis)
                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                           0;
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Best Local S
Matches 231
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13-AUG-1993;
24-AUG-1993;
19-NOV-1993;
03-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                          A cDNA library from the human stromal cell line 29SV48, in pME18S, was screened with an 800 bp fragment derived from mouse clone T118. This fragment encompasses the coding region conserved between two mouse clones, T118 and T110. Approx. 20 positive clones were selected and partially sequenced. Two clones, S86 and S109, were found to be approx. 75% homologous to the mouse clones over the first 163 AAs. Clone S86 continued to show homology to T110 until the stop codon, although to a lesser degree, for an overall homology of 65%. Clones T118 and clone of the character of the codon of the codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INRM )
                                                                                                                                                                                                                                                                                                     $109 do not show homology to each other or to the other clones after mouse residue 163 (human residue 160). An additiona mouse clone designated MBB has a 29 AA insert at the junction between the common and divergent portions of the mouse ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; page 79-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New ligand for the Flt3 tyrosine kinase receptor - and related nucleic acid, vectors, host cells and antibodies, useful for treating abnormal cell physiology and proliferation, e.g. cancer, also for diagnosis and drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Birnbaum D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-MAY-1993;
07-JUL-1993;
                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-MAY-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Flt3 ligand; tyrosine kinase receptor ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse MoT110/T118 Flt3 ligand peptide fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-AUG-1995
               181
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                                                                                                                                                                                                                                 Local Similarity
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DB; AAQ79464.
ELPEPRPRQ-LLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP
                                                                                                                                                                         MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
                                                         LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
                                                                                                                 VAVNLQDEKHCKALMSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                           MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
                                           LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
                                                                                                   VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INST NAT SANTE & RECH MEDICALE SCHERING CORP.
                                                                                                                                                                                                                                                                             232 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Culpepper
                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93US-0112391.
93US-0155111.
93US-0162413.
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93US-0106340.
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93US-0089263.
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                                                                                                                                                                                                                              99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90pp; English.
                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hannum CH,
                                                                                                                                                                                                                   Score 1212.5; DB Pred. No. 6e-114; 0; Mismatches
                                                                                                                                                                                                                                                DB 16;
                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                  232;
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                                                                        180
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181

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RESULT 5
AAB20189
ID AAB2
         be used for the prophylactic and/or therapeutic treatment of:
(a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis and C in humans), parasitic (e.g. malaria) and fungal infections (b) autoimmune diseases (e.g. rheumatoid arthritis and osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
                                                                                                                                                                                                          administering in vivo, into a tissue of a vertebrate, a Flt-3 ligand-encoding polynucleotide, and 1 or more antigen or ovtokine-encoding polynucleotides. The Flt-3 ligand-encoding
                                                                                      antigens or cytokines is produced in vivo. Pharmaceutical compositions comprising the polynucleotides are useful for suppressing tumour growth in a mammal. The tumour is melanoma glioma or lymphoma, particularly B-cell lymphoma. They can all
                                                                                                                                               the cells of the vertebrate in vivo, and a prophylactically or therapeutically effective amount of Flt-3 ligand and 1 or more
                                                                                                                                                                              polynucleotide may encode the present sequence or the mature polypeptide. The polynucleotides are incorporated into
                                                                                                                                                                                                                                                                                                                                                Immunogenic compositions comprising Flt-3 ligand encoding polynucleotide and one or more antigen, or cytokine encoding polynucleotides, useful for suppressing tumour growth and for treating autoimmune diseases (e.g. rheumatoid arthritis) -
                                                                                                                                                                                                                                                          immune response of a vertebrate to an antigen or a cytokine by
                                                                                                                                                                                                                                                                                                                        Claim 2; Page 125-126; 149pp; English.
                                                                                                                                                                                                                                                                                (Flt-3 ligand).
                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAF30307
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-123319/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (VICA-) VICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Flt-3 ligand; Fms-like tyrosine kinase; mouse; vaccine; immunotherapy; therapy; tumour; cancer; melanoma; glion lymphoma; autoimmune disease; infection; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse Flt-3 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB20189
                                                                                                                                                                                                                                                                          present sequence is that of mouse Fms-like tyrosine kinase t-3 ligand). The invention is directed to enhancing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELPEPRPRQLLLLLLLLLTTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000WO-US20679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0146170
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213..232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Signal_peptide 28..232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Extracellular_domain
   of these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytoplasmic_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232
diseases
                                           infections;
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RESULT 6
AAU02129
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                                                                                                                                   New chimeric polypeptide,
carboxy terminal fragment
cytoplasmic translocation
antigenic polypeptide -
                                                                                                                                                                                          WPI;
                                                                                                             Claim 9;
                                                                                                                                 antigenic
                                                                                                                                                                                                                                                        20-OCT-1999;
09-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                       Mouse; granulocyte-macrophage-colony stimulating factor; GM chimeric; heat shock protein; HSP; Flt-3 ligand; FL; exotox: ETA dII; antigenic; immunogenic; cytotoxic T cell response;
                                                                                                                                                                                                              Wu T,
                                                                                                                                                                                                                                                                                         20-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                           Unidentified.
                                                                                                                                                                                                                                                                                                                                                                             ETA dII; antigenic; imm vaccine; immunotherapy.
                                                                                                                                                                                                                                   (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
                                                                                                                                                                                                                                                                                                                                     WO200129233-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                   Flt-3 ligand (FL) used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU02129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU02129 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT 60
                                                                                                                                                                                        2001-290921/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELPEPRPRQ-LLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELPEPRPRQLLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \tt LRFVQTNISHLLKDTCTQLLGLKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230;
                                                                                                         Fig 19; 110pp;
                                                                                                                                 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232
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                                                                                                                                                                                                                                                        99US-0421608
2000US-0501097
                                                                                                                                                                                                                                                                                         2000WD-US41422
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.8%;
99.1%;
                                                                                                          English.
                                                                                                                                         useful as anti-tumour vaccines, comprises of heat shock protein, Flt-3 ligand or domain of Pseudomonas exotoxin A and
                                                                                                                                                                                                                                                                                                                                                                                                                                  make chimeric immunogenic polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       288
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Pred. No. 1.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                   factor; GM-CSF;
FL; exotoxin A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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used in construction of a chimeric polypeptide comprising: (a) a first polypeptide domain containing a carboxy terminal fragment of a heat shoc protein (HSP), an Fit-3 ligand (FL), a cytoplasmic translocation domain of a Pseudomonas exotoxin A (ETA dII), or a granulocyte-macrophage color stimulating factor (GM-CSF); and (b) a second polypeptide domain containing an antigenic polypeptide. A composition comprising the chimeric polypeptide is useful for inducing an immune response such as a

a heat shock

colony

inducing

such

The sequence represents the amino acid sequence of Flt-3 ligand (FL)

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QY
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Best Local S
Matches 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric polypeptide present in the composition is administered as naked DNA by gene gun or equivalent, or by liposomal formulation. These are thus useful for vaccinating a mammal against infection by inducing an immune response to a pathogen. Preferably they are useful for vaccinating a mammal against a tumour antigen. The compositions and methods are useful for stimulating or enhancing the immunogenicity of a selected antigen or stimulating or enhancing a cellular immune response specific for that antigen. The chimeric nucleic acid molecules and vaccination methods, yield potent antigen-specific immunotherapy. The polynucleotides and DNA vaccines can induce a cellular immune response that is at least 40 fold more potent than conventional DNA vaccines. The vaccines are safe and useful for administration to domesticated or agricultural animals, as well as humans, and have low immunogenicity.
                                                                                                                                                                                                                                                                                                                                                     Flt-3 ligand; Fms-like tyrosine kinase; mouse; vaccine;
immunotherapy; therapy; tumour; cancer; melanoma; glion
lymphoma; autoimmune disease; infection; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB20187 standard; Protein; 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
WPI; 2001-123319/13.
N-PSDB; AAF30305, AA
                                                                                                                                     31-JUL-2000; 2000WO-US20679
                                                                                                                                                                    08-FEB-2001.
                                                                                                                                                                                                  WO200109303-A2
                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse Flt-3 ligand (secreted form).
                                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAY-2001 (first entry)
                                              Hermanson GG
                                                                                                         30-JUL-1999;
                                                                                                                                                                                                                                                                              Peptide
                                                                          (VICA-) VICAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LREVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288 AA;
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                                                                             INC
                                                                                                         99US-0146170
                                                                                                                                                                                                                            /label= Signal_peptide 28..189 /label= Mature_protein
                                                                                                                                                                                                                                                                          Location/Qualifiers
AAF30313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.3%;
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Pred. No. 5.3e-93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
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                                                                                                                                                                                                                                                                                                                                                                       glioma;
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The present sequence is that of a secreted form of mouse Fms-like CC tyrosine kinase (Flt-3 ligand), lacking the transmembrane and cytoplasmic domains of the full-length form (see AAB20186). This secreted form of the Flt-3 ligand is expressed by vector VR6200 (see AAB201313). The invention is directed to enhancing the immune response of a vertebrate to an antigen or a cytokine by administering in vivo, into a tissue of a vertebrate, a Flt-3 ligand-encoding polynucleotide, such as VR6200, and I or more antigen- or cytokine-encoding polynucleotides. The polynucleotides are incorporated into the cells of the vertebrate in vivo, and a prophylactically or therapeutically effective amount of Flt-3 (ligand and 1 or more antigens or cytokines is produced in vivo. Pharmaceutical compositions comprising the polynucleotides are ligand and 1 or more antigens or cytokines is produced in vivo. Pharmaceutical compositions comprising the polynucleotides are useful for suppressing tunour growth in a mammal. The tunour is melanoma, glioma or lymphoma, particularly B-cell lymphoma. The co-injection of VR6200 and tumour-specific antigen-encoding plasmid conjugation of the prophylactic and/or therapeutic treatment of: challenge. The claimed pharmaceutical compositions can also be used for the prophylactic and/or therapeutic treatment of: (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B can dc in humans), parasitic (e.g. malaria) and fungal infections; (c) cancer; and (d) Auleszky's disease in pigs. CC Various other examples of these diseases are given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunogenic compositions comprising Flt-3 ligand encoding polymuclectide and one or more antigen, or cytokine encoding polymuclectides, useful for suppressing tumour growth and for treating autoimmune diseases (e.g. rheumatoid arthritis) -
                                                                                   Various other examples of these diseases are given in the
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Sequence 189 AA;

specification.

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                                                                                                                                                                                                          Matches 189;
                                                                                                                                                                                                                                   Query Match
  181
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                                                   121
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                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                        Н
                                                                                                                                                                                 1 MTVLAPAWSPNSSLLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT 60
1 ELPEPRPRQ 189
|||||||||
1 ELPEPRPRQ 189
                                                                 LRFVQTNISHLLKDTCTQLLALKPCIGKACQNESRCLEVQCQPDSSTLLPPRSPIALEAT 180
                                                                                                                    VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
                                                                                                      VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                        LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT 180
                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                       82.1%;
100.0%;
                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                       Score 1004; DB 22;
Pred. No. 4.8e-93;
                                                                                                                                                                                                                                  Length 189;
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RESULT 8
AAB20191
ID AAB2
Flt-3 ligand; Fms-like tyrosine kinase; mouse; vaccine;
immunotherapy; therapy; tumour; cancer; melanoma; glion
lymphoma; autoimmune disease; infection; gene therapy.
                                                                                                                                   AAB20191;
                                                                                                                                                          AAB20191 standard; Protein; 172
           Mus musculus
                                                                                   Mouse Flt-3 ligand
                                                                                                         14-MAY-2001 (first entry)
                                               melanoma; glioma;
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RESULT 9
AAB2018E7
ID AAB20
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                                                                                                                                                                                                                                                                                                                                                                                                   polynucleotide may encode the present sequence or the mature the cells of the vertebrate in vivo, and a prophylactically or the reputically effective amount of Fit 3 ligand and 1 or more campositions comprising the polynucleotides are useful for compositions comprising the polynucleotides are useful for suppressing tumour growth in a mammal. The tumour is melanoma, caplioma or lymphoma, particularly B-cell lymphoma. They can also be used for the prophylactic and/or therapeutic treatment of:

(a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B and C in humans), parasitic (e.g. malaria) and fungal infections;

(b) autoimmune diseases (e.g. rheumatoid arthritis and osteoarthritis);

(c) Costeoarthritis); (c) cancer; and (d) Augeszky's disease in pigs.
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Best Local :
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Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of mouse Fms-like tyrosine kinase (Flt-3 ligand). The invention is directed to enhancing the immune response of a vertebrate to an antigen or a cytokine by administering in vivo, into a tissue of a vertebrate, a Flt-3 ligand-encoding polynucleotide, and 1 or more antigen- or cytokine-encoding polynucleotides. The Flt-3 ligand-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunogenic compositions comprising Flt-3 ligand encoding polynucleotide and one or more antigen, or cytokine encoding polynucleotides, useful for suppressing tumour growth and for treating autoimmune diseases (e.g. rheumatoid arthritis) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-123319/13.
N-PSDB; AAF30309.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytokine-encoding polynucleotides.
                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                           specification.
                AAB20188 standard;
                                                                                                                                                                                                                                                                                                                                                                                         Various other examples of these diseases are given in the
                                                                                             121
                                                                                                                                                                        61 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
                                                                                                                                                                                                                  Local Similarity
                                                                                             LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDRVSL 168
                                                                                                                          LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTL 168
                                                                                                                                                         VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                                                                                                 165;
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                                                                                                                                                                                                                                                                                                                                               172 AA;
                                                                                                                                                                                                                                                                                  Conservative
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                   Protein; 220
                                                                                                                                                                                                                                                                                               71.9%;
                                                                                                                                                                                                                                                                               ; Score 879; DB
; Pred. No. 1.7e
1; Mismatches
                                                                                                                                                                                                                                                                                                 879;
No. 1.
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1.7e-80;
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61

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VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120

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cc immune response of a vertebrate to an antigen or a cytokine by cc administering in vivo, into a tissue of a vertebrate, a Fit-3 crytokine-encoding polynucleotide, and 1 or more antigen- or cytokine-encoding polynucleotides. The Fit-3 ligand-encoding cytokine-encoding polynucleotides are incorporated into polynucleotide. The polynucleotides are incorporated into cytokine-encoding polynucleotides are incorporated into cytokines in polynucleotides are incorporated into cytokines in polynucleotides are incorporated into cytokines is produced in vivo. Pharmaceutical compositions comprising the polynucleotides are useful for suppressing tumour growth in a mammal. The tumour is melanoma, cytokines is produced in vivo. Pharmaceutical cylioma or lymphoma, particularly B-cell lymphoma. They can also be used for the prophylactic and/or therapeutic treatment of: C(a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B cand C in humans), parasitic (e.g. malaria) and fungal infections; C(b) autolumune diseases (e.g. rheumatoid arthritis and content of content con
Matches
                                          Query Match
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immunotherapy; therapy; tumour; cancer; melanoma; glion
lymphoma; autoimmune disease; infection; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenic compositions comprising Flt-3 ligand encoding polynucleotide and one or more antigen, or cytokine encoding polynucleotides, useful for suppressing tumour growth and for treating autoimmune diseases (e.g. rheumatoid arthritis) -
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N-PSDB; AAF30306.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hermanson GG
                                                                                            Sequence
                                                                                                                                         specification.
                        Local
al Similarity
177; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 123-124; 149pp; English.
                                                                                            220 AA;
  Conservative
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                      71.9%;
Score 879; DB 22;
Pred. No. 2.4e-80;
5; Mismatches 21;
                                                 Length 220;
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immune response of a vertebrate to an antigen or a cytokine by calministering in vivo, into a tissue of a vertebrate, a Fit-3 calministering in vivo, into a tissue of a vertebrate, a Fit-3 calministering polynucleotide, and I or more antigen or cytokine-encoding polynucleotides. The Fit-3 ligand-encoding cytokine-encoding polynucleotides. The Fit-3 ligand-encoding polynucleotides are incorporated into the vertebrate in vivo, and a prophylactically or the cells of the vertebrate in vivo, and a prophylactically or compositions comprising the polynucleotides are useful for compositions comprisition that in a mammal. The tumour is melanoma, comprising the polynucleotides are useful for compositions comprisition that is melanoma, comprising the polynucleotides are useful for compositions and for the tumour is melanoma, compositions compositions and for the tumour is melanoma, compositions compositions and for the tumour is melanoma, compositions and for tumour is melanoma, compositions and for tumour is melanoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Flt-3 ligand; Fms-like tyrosine kinase; mouse; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB20190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hermanson GG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (VICA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lymphoma; autoimmune disease; infection; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse Flt-3 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB20190 standard; Protein; 220 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunotherapy; therapy; tumour; cancer; melanoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPGNG---GPRAQHHGATR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEATELPEPRPRQLLLL-----LLLLPLTLVLLAA
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DB; AAF30308.
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                                                                                                                                                                                                                                                                                                                                                                                                                    2; Page 128; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VICAL INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first
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28..220
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/label= Mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treating
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RESULT 11
AAY58204
ID AAY58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 177; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
Sequences AAY58204 and AAY58206-Y58209 resepctively represent encoded, mature, clone 1 and clone 19 canine Fit-3 ligand, while sequences AAY5820-Y58211 represent encoded and mature feline Fit-3 ligand. The invention relates to canine interleukin-4 (IL-4), canine or feline Fit-3 ligand, canine or feline CD40, canine or feline CD54 (CD40 ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha) and feline granulocyte macrophage colony stimulating factor (GMCSF), and nuclecides which encode these immunoregulatory proteins. The proteins, their associated nucleic acids, specific antibodies and inhibitors may be used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (b) autoimmune diseases (e.g. rheumatoid arthritis and
osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
Various other examples of these diseases are given in the
                                                                                                                                                                       Claim 3b; Page 159-160;
                                                                                                                                                                                                 Nucleic acids encoding immunoregulatory proteins from cats or dogs, useful for treating or preventing e.g. tumors or autoimmune disease
                                                                                                                                                                                                                                                                                             Sim G,
                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9961618-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Canine Flt-3 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY58204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY58204 standard; Protein; 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specification.
                                                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                                                                                                                                        29-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                    28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                     02-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Flt-3 ligand; antibody; canine; feline; inhibitor; immune response;
                                                                                                                                                                                                                                                                                                                           (HESK-) HESKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mmunoregulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178
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                                                                                                                                                                                                                                               2000-072623/06.
DB; AAZ55487, AAZ55488, AAZ55489, AAZ55490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LREVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRS----PIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LTATALLTVCPGLLLPLVGTSHMFFLPYFLSFLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEATELPEPRPRQLLLL----LLLLPLTLVLLAA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPGNG---GPRAQHHGATR 177
                                                                                                                                                                                                                                                                                           Yang S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                            CORP
                                                                                                                                                                                                                                                                                                                                                        98US-0087306
                                                                                                                                                                                                                                                                                                                                                                                    99WO-US11942
                                                                                                                                                                                                                                                                                             Dreitz MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumour; cancer; autoimmune disease; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.9%;
                                                                                                                                                                     264pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>ن</u>
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Pred. No. 2.
                                                                                                                                                                                                                                                                                             Wonderling RS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22;
2.4e-80;
nes 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176
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RESULT 12
AAR66175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccines for therapeutic or prophylactic regulation of an immune response in animals (particularly cats, dogs, horses and humans). They may be used to treat autoimmune or infectious diseases including allergies, tumours, inflammation and graft rejection, and to increase the response from a co-administered antigen. The nucleotide sequences can also be used for the recombinant production of a protein, while nucleotide fragments are useful as probes, as amplification primers an as sources of inhibitory therapeutics (e.g., antisense oligonucleotides). The proteins may be used to raise antibodies and to screen for modulators of activity, while the antibodies may be used in detection, and in drug targetting.
                                                                                                                                                                                                   16-JUL-1993;
13-AUG-1993;
24-AUG-1993;
19-NOV-1993;
03-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR66175 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Flt3 ligand;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-AUG-1995
                                                                                                                                               (INRM
                                                                                                                                                                                                                                                                                             19-MAY-1993;
07-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                   18-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                       24-NOV-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                           WO9426891-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human S86/S109 Flt3 ligand peptide sequence
nucleic acid, vectors,
   New ligand for the Flt3 tyrosine kinase receptor - and related nucleic acid, vectors, host cells and antibodies, useful for
                                                       WPI; 1995-006787/01
N-PSDB; AAQ79642.
                                                                                                               Birnbaum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALPAPQAPR---LLLLLLPVALLLMSTAWCLHWRRRRRRRSPYPG
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                                                                                                                                                 INST NAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         294 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tyrosine kinase receptor ligand
                                                                                                             Culpepper
                                                                                                                                                                                                     93US-0065231.

93US-0089263.

93US-0092549.

93US-0106340.

93US-0112391.

93US-0155111.

93US-0162413.
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                                                                                                                                                 SANTE & CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide;
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                                                                                                               JA,
                                                                                                                                                                    RECH MEDICALE
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Pred. No. 1.3e-69;
3; Mismatches 38;
                                                                                                               Hannum CH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ΑA
                                                                                                                  Lee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 294;
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В QΥ В Ωy 망 80

Вþ δÃ

08-FEB-2001

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RESULT 13
AAB20194
ID AAB20194
AC AAB20
XX AB20
XX IAMAD
DT 14-MA
DE Human
XX Flt-3
KW Inmur
KW Imph
XX Inmur
KW Imph
CS Homo
XX Homo
CX Homo

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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pME188, was screened with an 800 bp fragment derived from mouse clone T118. This fragment encompasses the coding region conserved between two mouse clones, T118 and T110. Approx. 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 76-77; 90pp; English.
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immunotherapy; therapy; tumour; cancer; melanoma; gliom
lymphoma; autoimmune disease; infection; gene therapy.
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27...235
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/label= Transmembrane_domain
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Pred. No. 1.4
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Matches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ligand-encoding polynucleotide, and 1 or more antigen- or cytokine-encoding polynucleotides. The F1t-3 ligand-encoding polynucleotides. The F1t-3 ligand-encoding polynucleotides are fitted from the polynucleotide may encode the present full-length human F1t-3 ligand polypeptide, or amino acids 27-185, 1-185, 27-235 or 1-235 or fitted fitted from the fitt-3 ligand. The polynucleotides are incorporated into the cells of the vertebrate in vivo, and a prophylactically or therapeutically effective amount of F1t-3 ligand and 1 or more antigens or cytokines is produced in vivo. Pharmaceutical compositions comprising the polynucleotides are useful for suppressing tumour growth in a mammal. The tumour is melanoma, glioma or lymphoma, particularly B-cell lymphoma. They can also be used for the prophylactic and/or therapeutic treatment of:

(a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B and C in humans), parasitic (e.g. malaria) and tingal infections;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 200
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is that of human Fms-like tyrosine kinase (Flt-3 ligand). The invention is directed to enhancing the immune response of a vertebrate to an antigen or a cytokine by administering in vivo, into a tissue of a vertebrate, a Flt-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (b) autoimmune diseases (e.g. rheumatoid arthritis and
osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs
Various other examples of these diseases are given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 137-138; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenic compositions comprising Flt-3 ligand encoding polynuclectide and one or more antigen, or cytokine encoding polynuclectides, useful for suppressing tumour growth and for treating autoimmune diseases (e.g. rheumatoid arthritis) -
                      05-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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DB; AAF30312.
                                                                                                                                                                                                                                                                                                                                                                               VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
                                                                                                                                                                                                                                                                                               LRFVQTNISRLLQETSEQLVALKPWITR - - QNFSRCLELQCQPDSSTLPPPWSPRPLEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000WO-US20679
                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 772.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; DB 22;
1.4e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                             60
                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                   Local
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25-AUG-1993;
03-DEC-1993;
07-MAR-1994;
11-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                            A human T-cell lambda-gtl0 random primed cDNA library was screened with a fragment corresponding to the extracellular domain of mouse fit3 ligand (flt3-L) (nt 103-516 of AAQ79076) to isolate human flt3-L cDNA. Flt-3 stimulates progenitor and stem cells, and can be used e.g. in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 29-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated ligands for flt 3 receptors - anaemia, AIDS and various cancers {\bf r}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Flt-3 ligand; flt3-L; anemia; cancer; AIDS; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beckmann MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-AUG-1993
                  121 LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT 180
                                                                                                                                                                                                                                                   1 MTVLAPAWSPNSSLLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
                                                                                                                                                                       VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1995-008071/02
                                                                                                                                                                                                                          MTVLAPAWSP-TTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVT
APTAPOPP -- LLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSP
                                                                       LRFVQTNISRLLQETSEQLVALKPWITR-
                                                                                                                                                 VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC
                                                                                                                                                                                                                                                                                                      al Similarity
163; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ79079
                                                                                                                                                                                                                                                                                                                                                                              235 AA;
                                                                                                                                                                                                                                                                                                      Conservative
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93US-0162407.
94US-0209502.
94US-0243545.
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93US-0106463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94EP-0303575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Transmembrane_domain
206..235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "extracellular domain position 28"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Extracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label=_Sig_peptide
                                                                                                                                                                                                                                                                                                                    62.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytoplasmic_domain
                                                                                                                                                                                                                                                                                                  Score 768.5; DB 1
Pred. No. 3.6e-69;
7; Mismatches 43
                                                                       -QNFSRCLELQCQPDSSTLPPPWSPRPLEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful
                                                                                                                                                                                                                                                                                                                                         DB 16;
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                                                                                                                                                                                                                                                                                                                                         Length
                                    228
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RESULT 15
AAW67769
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                                                                                   Qγ
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                                                                                                                                                                                                                                                                                                                    A method has been developed of initiating or enhancing: (i) an antigen-
CC specific immune tolerance; or (ii) immunotolerance of a therapeutic
CC immunogenic molecule by addition of a polypeptide, before, after or with
CC immunogenic molecule by addition of an oplypeptide, before, after or with
CC the mucosal administration of an immunotolerising amount of the antigen
CC or therapeutic molecule, respectively. The polypeptide is capable of
CC ligand (flt3-L), where x is an amino acids 28-x of murine flt3
CC acids 28-y of human flt3-L, where y is an amino acid between 163-231; b) amino
CC and c) a polypeptide that has at least 90% identity to the polypeptides
CC of either (a) or (b). The method ameliorates the effects of autoimmune
CC diseases, food allergies or organ or tissue rejection following
CC transplantation. Administration of flt3-L allows lower doses of antigens
CC to be used in vivo for mucosally administered antigens. The present
                        γ
                                                       DЬ
                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 163; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW67769 standard; Protein; 235 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antigen-specific peripheral immune tolerance; flt3-ligand; flt3-L; immunogenic; autoimmune disease; organ transplantation; food allergy; tissue transplantation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW67769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 14-15; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methods for initiating or enhancing antigen specific immune tolerance - by using murine or human flt3 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09857655-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human flt3-ligand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUN-1997;
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                                                                                                                                                                                                                                                                                             Sequence
178 APTAPQPP--LLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSP 227
             1 ELPEPRPROLLLLLLLLPLTLYLLAAAWGLRWQRARRR-----GELHPGVPLP 228
                                                          120
                                                                        121 LREVOTNISHLIKDTCTOLLALKPCIGKACQNESRCLEVQCQPDSSTLLPPRSPIALEAT 180
                                                                                                                  MTVLAPAWSPNSSILLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
                                                                                                                                                                           235 AA;
                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                              62.8%;
70.3%;
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                                                                                                                                                                                                                                    ; Score 768.5; DB 2; Pred. No. 3.6e-69; 17; Mismatches 43
                                                                                                                                                                                                                                                                  DB 20; Length 235;
                                                                                                                                                                                                                                        43;
                                                                                                                                                                                                                                        Indels
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Search completed: November 24, 2002, 10:10:13 Job time : 32.2296 secs

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Result
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published_Applications_AA: *
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Listing first 45 summaries
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/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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     US-09-448-378-1
US-09-983-806-6
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US-09-904-536-14
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Sequence 10, Appli
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Sequence 11, Appli
Sequence 18, Appli
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Sequence 17, Appli
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US-09-793-139-4	US-09-867-550-2026	US-10-052-586-414	US-09-989-721-57	US-09-990-456-57	US-09-993-604-57	US-09-991-163-57	US-09-990-442-57	US-09-991-073-57	US-09-989-732-57	US-09-989-731-57	US-09-989-727-57	US-09-989-279-57	US-09-989-723-57	US-09-989-722-57	US-09-187-368-1	US-09-992-598-57	US-09-987-107-35	US-09-800-729-208	US-09-211-755B-47	US-09-818-879-47	US-09-793-139-47		US-09-867-852-2	US-09-948-018-2	US-09-867-852-142
Sequence 4, Appli		Sequence 414, App	Sequence 57, Appl		Sequence 57, Appl	Sequence 57, Appl	57,	Sequence 57, Appl	Sequence 57, Appl	•	Sequence 57, Appl	Sequence 57, Appl	Sequence 57, Appl	57,	Sequence 1, Appli	Sequence 57, Appl	Sequence 35, Appl	208,	Sequence 47, Appl	Sequence 47, Appl	17,	26,	Sequence 2, Appli	Sequence 2, Appli	Sequence 142, App

### ALIGNMENTS

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US-10-095-449-2
; Sequence 2, Application US/10095449
; Batent No. US2020160004A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 1
                                               ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTMARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
REFERENCE/DOCKET NUMBER: 2813-C TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lyman, Stewart D.

Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER
                                                                                                                 APPLICATION NUMBER: US/08/162,407
FILLING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILLING DATE: August 25, 1993
APPLICATION NUMBER: 08/106,463
FILLING DATE: August 12, 1993
APPLICATION NUMBER: 08/068,394
FILLING DATE: May 24, 1993
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/10/095,449 FILING DATE: 13-Mar-2002 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/669,692 FILING DATE: 24-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Stephen L. Malaska, STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Washington
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                                               32,655
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TELEFAX: (206) 233-0644

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US-09-983-8¢5-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 2
LENGTH: 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09448378 Patent No. US20020034517A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 231; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/448,378 CURRENT FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Brasel, Kenneth
TITLE OF INVENTION: Dendr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                       181 ELPEPRPRQLLLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP 231
                                                                                                         181
                                                                                                                                        121
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                                                                                                                                                      121 LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLEPRSPIALEAT 180
                                                                                                                                                                                                      61
                                                                                                                                                                                                                   61 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.0%; es 231; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                        ELPEPRPRQLLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP 231
                                                                                                                                     LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
                                                                                                                                                                                                   VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELPEPRPRQLLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn version 3.0
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                                                                                                                                                                                                                                                                                                                              100.0%; Score 1223; DB 10; ilarity 100.0%; Pred. No. 1.5e-107; Conservative 0; Mismatches 0;
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; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-983-806-2
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                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
181
                                       181 ELPEPRPRQLILLILLIPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP 231
                                                                                 121
                                                                                                     121 LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
                                                                                                                                                                  61 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                          61 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                        1 MTVLAPAWSPNSSLLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
                                                                                                                                                                                                                                                                           1 MTVLAPAWSPNSSILLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 2813-C TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lyman, Stewart D.
Beckmann, M. Patricia
ELPEPRPRQLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP
                                                                               LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/162,407 FILING DATE: 03-DEC-1993 APPLICATION NUMBER: 08/111,758 FILING DATE: August 25, 1993 APPLICATION NUMBER: 08/106,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 231 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 25-Oct-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: Apple Macintosh 7 OPERATING SYSTEM: Macintosh 7 SOFTWARE: Microsoft Word, Ver:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 32,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Malaska, Stephen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/444,626 FILING DATE: 19-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Washington COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Stephen L. Malaska, STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1223; DB 10; ilarity 100.0%; Pred. No. 1.5e-107; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-oct-2001
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231
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RESULT 4

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US-10-095-449-6
; Sequence 6, Application US/10095449
; Patent No. US20020160004A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                   US-10-095-449-6
                                                                                                                                                                                                                                                                                                                      Matches 163;
                                                                                                                                                                                                                                                                                                                                         Best
                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
121
                                                                                                                                                           60 VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC 119
                                                                                                                                                                                  61 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                             1 MTVLAPAWSPNSSLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lyman, Stewart D.

Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                              LRFVQTNISRLLQETSEQLVALKPWITR--QNFSRCLELQCQPDSSTLPPPWSPRPLEAT
                                                                                                   LREVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT 180
                                                                                                                                                                                                                                          MTVLAPAWSP-TTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 24-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 13-Mar-2002 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/10/095,449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 235 amino acids
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                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                          (206) 587-0430
                                                                                                                                                                                                                                                                                                                                         62.8%;
70.3%;
                                                                                                                                                                                                                                                                                                                17; Mismatches
                                                                                                                                                                                                                                                                                                                                       Score 768.5; DB 9
Pred. No. 6.5e-65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #5.1
                                                                                                                                                                                                                                                                                                                      43;
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                                                                                  177
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; LENGTH: 235
; TYPE: PRT
; ORGANISM: HOMO Sapiens
US-09-448-378-1
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US-09-448-378-1
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US-09-983-806-6
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SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09448378 Patent No. US20020034517A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09983806 Patent No. US20020107365A1 GENERAL INFORMATION:
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Best Local Similarity
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CURRENT FILING DATE: 1999-11-23
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 APTAPQPP--LLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSP 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 ELPEPRPROLLLLLLLLPLTLVLLAAAWGLRWQRARRR----GELHPGVPLP 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 LRFYQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MTVLAPAWSP-TTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
                                                                                                                                                      PRIOR APPLICATION DATA
                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/983,806
                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lyman, Stewart D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRFVQTNISRLLQETSEQLVALKPWITR--QNFSRCLELQCQPDSSTLPPPWSPRPLEAT
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                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version
                                                                                                                                                                         FILING DATE: 25-Oct-2001
CLASSIFICATION: 530
APPLICATION NUMBER: 08/111,758 FILING DATE: August 25, 1993 APPLICATION NUMBER: 08/106,463 FILING DATE: August 12, 1993
                                                                                                               APPLICATION NUMBER: US/08/444,626 FILING DATE: 19-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                              STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
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                                                                        APPLICATION NUMBER: US 0 FILING DATE: 03-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Stephen L. Malaska
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn version 3.0
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Pred. No. 6.5e-65;
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                                                                                              08/162,407
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ATTORNEY/AGENT INFORMATION:

APPLICATION NUMBER: 08/068,394 FILING DATE: May 24, 1993

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                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 235
                                                                                                                                     Matches
                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09904536 Patent No. US20020111475A1
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                                                                                                                                                                                                                                    TYPE: PRT
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 APTAPQPP--LLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSP 227
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                                                                                                                                                    Local
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MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                             SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRFVQTNISRLLQETSEQLVALKPWITR--QNFSRCLELQCQPDSSTLPPPWSPRPLEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT 60
                                                                                                                                       163;
                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Malaska, Stephen L. REGISTRATION NUMBER: 32,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 235 amino acids
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                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                               62.8%; Score 768.5; DB 170.3%; Pred. No. 6.5e-65;
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Pred. No. 6.
                                                                                                                                  Mismatches
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                                                                                                                                                                 DB 10;
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                                                                                                                                   43;
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                                                                                                                                  Indels
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                                                                                                                              Gaps
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; ORGANISM: Homo sapiens US-09-904-536-10
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; TYPE: PRT
; ORGANISM: Murine
US-09-904-536-19
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US-09-904-536-19
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                                                                                                                                  SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 212
 Query Match
Best Local Similarity
Matches 144; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/09904536 Patent No. US20020111475A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 136; Conserv
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19, Application US/09904536 Patent No. US20020111475A1
                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/904,536 CURRENT FILING DATE: 2001-07-16
                                                                                                                                                                                                                                                                                       APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: PLT3-TL MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100 PRIOR FILING DATE: 1999-07-02
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                                                                                                                    TYPE: PRT
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   Conservative
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99.3%;
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 Score 692; DB
Pred. No. 8.5e
15; Mismatches
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Pred. No. 4.3e-61;
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 DB 10;
3.5e-58;
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Best Local Similarity
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
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       APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLI3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
GURRENT APPLICATION NUMBER: US/09/904,536
GURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
ROSENERS DESCRIPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MCGICW, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
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TYPE: PRT
SOFTWARE: PatentIn Ver.
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                                                                                                                                                                                                                                                                                                                                         WGLRWQRARRR----GELHPGVPLP 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPECLRFVQTNISHLLKDTCTQLLALKPCIG 147
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Pred. No. 2.4e-57;
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RESULT 13
US-09-904-536-16
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US-09-904-536-18
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LENGTH: 209
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Best Local :
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                                                                                                                                                                                                                                                                                                            Matches 143;
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: U$\0,09\/904\,536
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                             177 WCLHWQRTRRRTPRPGEQVPPVPSP
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Pred. No. 3e-57;
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Sequence 16, Application US/09904536 Patent No. US20020111475A1

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PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
SOFTMARE: Patentin Ver. 2.1
SEQ ID NO 16
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APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
                                                                                                                                                                                                          Best Local Similarity Matches 142; Conserv
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
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CURRENT FILING DATE: 2001-07-16
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
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CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
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US-09-629-430B-23	-08-486-661-34	-08-484-882-3	-472-1	-261-553-3	-08-162-413-	-08-155-111-	-10-262-439	-10-218-6	-09-451-527	-09-322-4	791-537-1	629-430B	629-430B-	791-537-1	$\vdash$	-080	-09-629-4	-US02	-09-501-0	01-0	-09-791-53	-09-629-43	S-09-791-53	-08-486-661	-08-484-882	08-472-168	-08-261	-08-162-413	8-155-111	-60-368-26	-10-09	98	-09-62	-09-441	S-08-877-421-	S-08-669-692-	-08-444-6	26-
Sequence 23, App1	34, Ap	34,	34,	Sequence 34, Appl	34,	34,	equence 7,	e 7,	equence $\overline{7}$ ,	e 7,	1220	e 15,	11,	1857	-	20,	е 9,	18,	25,	25,	5162	13,	e 867	38,	38,	e 38,	38,	equence 38,	38,	e 2,	e 2,	e 2,	e 8,	e 2,	e 2, Appl	ce 2,	2, Appl	equence 2,

# ALIGNMENTS

PCT-US98-12085-2 RESULT 1

Sequence 2, Application PC/TUS9812085 GENERAL INFORMATION:

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM/PC Compatible
COMPUTER: IBM/PC Compatible
COMPUTER: Word for Windows 95
SOFTWARE: Word for Windows 95, Version 7.(
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/12085
FILING DATE: 12-JUN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
PROTECTION OF THE PORT OF TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: IMMUNEX CORPORATION
TITLE OF INVENTION: A Method of Enhancing Antigen-Specific Peripheral Immune NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                              REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 51 Uni
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       TELEPHONE:
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(206) 587-0430
                                                                                                                                                             2855-WO
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Sequence

TELEX: 756822
INFORMATION FOR SEQ ID NO:

2

TELEFAX: 12.

(206) 233-0644

SEQUENCE CHARACTERISTICS:

LENGTH:

amino acids

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RESULT 2
US-08-068-394-2
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Query Match
Best Local Similarity
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Best Local Similarity
Matches 231; Conserv
                                                                                                          TELEX: 756822
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                            MOLECULE TYPE:
                                                                                                                                                      TELEPHONE: (206) 587-0430
TELEPHONE: (206) 233-0644
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compostible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                       · SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 4
                                                -068-394-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lyman, Stewart D. APPLICANT: Beckmann, M. Patr
                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION: .
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                                                                           TOPOLOGY:
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                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 199305
                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                     CITY:
                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                               Street
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     Score 1223;
Pred. No. 3.
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Pred. No. 3.5e-110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunex Corporation
     DB 4;
3.5e-110;
               Length 231;
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenth Release #1.0, Version #1.25
                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 6
121 LREVQTNISHLIKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                      61
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                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                  TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Seattle
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                                                                 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
                                                VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
                                                                                                               {\tt MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington
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51 University Street
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                            (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19930812
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                                                                                                                                                                                             Score 1223; DB 5;
Pred. No. 3.5e-110;
                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 28.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEPAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/060 FILING DATE: May 24, 1993 ATTORNEY/AGENT INFORMATION: NAME: Malaska, Stephen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: August 2
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (22
TELEFAX: 756822
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CITY: S
                 181 ELPEPRPRQLLLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP 231
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                                                                                                                                              61 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                 61 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
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                                                                                           LREVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT 180
 ELPEPRPRQLLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP
                                                                        LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
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DN: 435
                                                                                                                                                                                                                                                                                                          100.0%; Score 1223; DB 5; 100.0%; Pred. No. 3.5e-110;
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RESULT 5
US-08-162-407-2
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GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                      Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 231; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh 7.0.1
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
PRIOR APPLICATION NUMBER: 08/06,463
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
ATTORNERY/ACENT INFORMATION:
NAME: Malasks Stanhon I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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                 181 ELPEPRPRQLLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPCVPLPSHP 231
                                                                         121 LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
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REFERENCE/DOCKET NUMBER: 2813-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Malaska, Stephen L. REGISTRATION NUMBER: 32,6
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE:
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ELPEPRPRQLLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP
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Pred. No. 3.5e-110;
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RESULT 6 US-08-444-625-2

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RESULT 7
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Best Local Similarity
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FILLING DATE: August 25, 1993
PRIOR APPLICATION DATA: 08/106,463
APPLICATION UNMBER: 08/106,463
FILLING DATE: August 12, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA: 08/068,394
FILLING DATE: May 24, 1993
CLASSIFICATION NUMBER: 08/068,394
FILLING DATE: May 24, 1993
CLASSIFICATION: 424
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OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,625
FILING DATE: 19-MAY-1995
                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION: NAME: Malaska, Stephen L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                      121 LREVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLDPRSPIALEAT 180
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CORRESPONDENCE ADDRESS:
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APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
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STREET: 51
Seattle
                                                                                                                                                                     61 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
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                                                                                                                                                                                                                                                                                                                                                                                                     linear
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Best Local 9
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463

FILING DATE: August 108/106,463
                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 587-0430
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
      181
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APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
                                     181
                                                                      121
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                                                                                                                                                   61 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Malaska, Stephen L. REGISTRATION NUMBER: 32,6 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/06; FILING DATE: May 24, 1993 CLASSIFICATION: 530
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ELPEPRPRQLLLLLLLLLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP 231
                    ELPEPRPRQLLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP 231
                                                                                  LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT 180
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                                                                 LREVQTNISHLLKDTCTQLLALKPCIGKACQNESRCLEVQCQPDSSTLLPPRSPIALEAT
                                                                                                                              VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
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TON: 530
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University Street
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                                                                                                                                                                                                                                                                              Score 1223; DB 8;
Pred. No. 3.5e-110;
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US-08-444-632-2
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APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/162,407
FILLING DATE: 03-DEC-1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintos
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                      121 LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT 180
                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
TYPE: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/100,***
APPLICATE: August 12, 1993
FILING DATE: August 12, 1993
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CITY: Seattle
STATE: Washington
                                   181 ELPEPRPRQLILLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP 231
                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Malaska, Stephen L. REGISTRATION NUMBER: 32,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: May 24, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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                                                                                                                                                                                                                                                                                   Match 100.0%; Score 1223; DB 8; Local Similarity 100.0%; Pred. No. 3.5e-110; es 231; Conservative 0; Mismatches 0;
                                                                                                                                                           VAVNLQDEKHCKALWSLELAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
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LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
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US-08-669-692-2
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GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
APPLICANT: INVENTION: Ligands for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/162,407
APPLICATION NUMBER: 08/11,758
APPLICATION NUMBER: 08/11,758
FILING DATE: August 25,1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12,1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24,1993
CLASSIFICATION: 530
                                                                                                                                                                                                                                                              Matches 231;
                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 1223; DB 10; Best Local Similarity 100.0%; Pred. No. 3.5e-110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
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MEDIUM TYPE: Floppy disk
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181
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                               181
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TELEFAX: (206) 233-0644
TELEX: 756822
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               ELPEPRPRQLLLLLLLLLLVLLAAAWGLRWQRARRRGELHPGVPLPSHP 231
                                                                LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT 180
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US-08-877-421-2
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GENERAL INFORMATION:
APPLICANT: Viney, Joanne L.
APPLICANT: Nowatt, Allan McI.
APPLICANT: Abbott, Nicholas
ITITLE OF INVENTION: A Method of Enhancing Antigen-Specific Peripheral Immune
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
Sequence 2, Application US/09448378
GENERAL INFORMATION:
APPLICANT: Brasel, Kenneth
TITLE OF INVENTION: Dendritic Cell Stime
FILE REFERENCE: 2836-D
CURRENT APPLICATION NUMBER: US/09/448,378
CURRENT FILING DATE: 1999-11-23
NUMBER OF SEO ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Flopy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Macintosh 7.6
SOFTWARE: Microsoft Word, Version #6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/877,421
FILING DATE: 17-JUN-1997
CLASSIFICATION: 514
AFTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 28.55
TELECOMMUNICATION INFORMATION:
TELEPHONDE: 4206 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 1223; DB 12; Best Local Similarity 100.0%; Pred. No. 3.5e-110;
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LENGTH: 231 amino acids
TYPE: amino acid
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CITY: Seattle
STATE: Washington
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(206) 233-0644
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                                                                   Dendritic Cell Stimulatory Factor
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US-09-983-806-2
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   Sequence 2, Application US/09983806 GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Mus
US-09-448-378-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 8
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                                                                                                                                                                                                                                                                                           Matches 231;
                                                                                                                                                                                                                                                                                                          Query Match 100.0%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/09629430E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/146,170
PRIOR FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/629,430B CURRENT FILING DATE: 2000-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hermanson, Gary George
TITLE OF INVENTION: FLT-3-Ligand-Encoding Polynucleotide at
TITLE OF INVENTION: Polynucleotide-Based Vaccine Enhancer
FILE REFERENCE: 1530.0130001
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                 181 ELPEPRPRQLLLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP 231
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                                                                                           LRFVQTNISHLLKCTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT 180
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Pred. No. 3.5e-110;
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; TOPOLOGY: linear; MOLECULE TYPE: Protein; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-983-806-2
                                   RESULT 14
US-10-095-449-2
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Sequence 2, Application US/10095449 GENERAL INFORMATION:
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/983,806
FILING DATE: 25-Oct-2001
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                     LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lyman, Stewart D.
Beckmann, M. Patricia
                                                                                                                                     ELPEPRPRQLLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP 231
                                                                                                                                                                                                                                                                                                    VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
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                                                                                                                   ELPEPRPROLLLLLLLLPLTLVLLAAAWGLRWQRARRGELHPGVPLPSHP 231
                                                                                                                                                                                                                                                                               VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: August 25, 1993
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/444,626 FILING DATE: 19-MAY-1995 APPLICATION NUMBER: US 08/162,407 FILING DATE: 03-DEC-1993 APPLICATION NUMBER: 08/111,758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Microsoft Word, Version #5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Stephen L. Malaska, Immunex Corporation STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Malaska, Stephen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
181 ELPEPRPROLLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP 231
                                                                            121 LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT 180
                                                                                                 121 LREVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT 180
                                    181 ELPEPRPRQLLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP 231
                                                                                                                                                             61 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
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                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                         1 MTVLAPAWSPNSSLLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 587-0430
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                                                                                                                                                                                                                                                                                                                            231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (200) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 231 amino acids
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REGISTRATION NUMBER: 32,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/162,407 FILING DATE: December 3, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/669,692 FILING DATE: 24-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/10/095,449 FILING DATE: 13-Mar-2002
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Pred. No. 3.5e-110;
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US-60-368-263-2

Sequence 2, Application US/60368263 GENERAL INFORMATION:

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Qy
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APPLICANT: Liebowitz, David N.
APPLICANT: Liebowitz, David N.
APPLICANT: Maliszewski, Charles R.
TITLE OF INVENTION: METHODS OF USING FLT-3 LIGAND IN IMMUNIZATION PROTOCOLS
FILE REFERENCE: 3399
CURRENT APPLICATION NUMBER: US/60/368,263
CURRENT FILING DATE: 2002-03-26
NUMBER OF SEO ID NOS: 4
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
SEQ ID NO 2
INVER: PAT
ORGANISM: Mus sp
US-60-368-263-2
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Search completed: November 24, 2002, 10:17:26 Job time: 136.328 secs
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                                                                181 ELPEPRPROLLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP 231
                                                                                    181 ELPEPRPRQLLLLLLLLLPLTLVLLAAAWGLRWQRARRRGELHPGVPLPSHP 231
                                                                                                                                 Gaps
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Minimum Maximum Title: Perfect score: OM protein - protein search, using sw model Database Post-processing: Minimum Match 0% Total number of hits satisfying chosen parameters: Scoring table: Searched: DB DB seq seq length: 0 length: 2000000000 US-09-448-378-1 1242 4 3 2 1 BLOSUM62 1 MTVLAPAWSPTTYLLLLLLL......RPGEQVPPVPSPQDLLLVEH 235 283224 seqs, 96134422 residues Gapop 10.0 , November 24, PIR\_73:\* Maximum Match Listing first GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compus pir1:\*
pir2:\*
pir3:\* Gapext 0.5 2002, 100% 45 su summaries 10:08:46 ; Search time 14.6245 Seconds (without alignments)
1544.781 Million cell updates/sec Compugen Ltd 283224

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

ţ	30	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	ω	2	1	No.	Result
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	106	418	1509	530	199	757	263	366	289	746	485	299	590	910	479	753	1386	238	793	387	474	661	1217	220	220	231	178	245	235	Length	
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### ALIGNMENTS

A; Molecule type: mRNA
A; Residues: 1-71,/a/,73-235 <HAN>
A; Residues: 1-71,/a/,73-235 <HAN>
A; Cross-references: GB:U04806; NID:9483844; PIDN:AAA17999.1; PID:9483845
A; Note: the authors translated the codon AGT for residue 25 as Met
C; Genetics: A;Cross-references: EMBL:U29874; NID:g1072036; PIDN:AAA90949.1; PID:g1072037
R;Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.;
felt, A.; Muench, M.; Kelner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik
Nature 368, 643-648, 1994
A;Title: Ligand for FIT3/FLK2 receptor tyrosine kinase regulates growth of haematopoi
A;Reference number: S43290; MUID:94195428; PMID:8145851
A;Accession: S43292
A;Status: preliminary A;Cross-references: EMBL:U03858; NID:949478; PIDN:AAA19825.1; PID:9494979 R;Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escoba Oncogene 11, 1165-1172, 1995 A;Title: Structural analysis of human and murine flt3 ligand genomic loci. A;Reference number: 139075; MUID:96032581; PMID:7566977 A;Accession: 139075
A;Status: preliminary; translated from GB/EMBL/DDBJ C; Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 01-Dec-2000 C; Accession: 138440; 139075; S43292 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-235 <RES> R;Lyman, S.D.; James, L.; Johnson, L.; Brasel, K.; de Vries, P.; Escobar, S.S.; Downe Blood 83, 2795-2801, 1994 C; Species: Homo sapiens (man) δÃ Вb δÃ В QY A; Molecule type: DNA A; Residues: 1-235 < RE2> A; Reference number: A; Accession: I38440 A;Title: Cloning of the human homologue of the murine flt3 ligand: a growth factor fo A;Reference number: I38440; MUID:94235842; PMID:8180375 A; Introns: 11/3; 48/3; 66/3; 114/3; 161/1; 220/3 flt3 ligand - human Best Matches Query Match 121 61 61 Local Similarity ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL 120 RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT A SNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLConservative 100.0%; 0; Score 1242; DB 2; Pred. No. 5.4e-99; 0; Mismatches 0; Indels Length 235; 0; Gaps Escobar, 120 180 0; ŝ

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C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C:Accession: I39076
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A; Accession: $43293
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A;Introns:
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                                                                                                                                                                                                                                                                                                                                                                                   A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: Structural analysis of human and murine flt3 ligand A; Reference number: 139075; MUID:96032581; PMID:7566977
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A; Residues: 1-245 < HAN>
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       #TVLAPAWSPTTYLLLLLLLSGLSGTODCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
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                                                                                                                                Conservative
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100.0%;
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Pred. No. 3.
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Pred. No. 1.2e
7; Mismatches
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A; Title: Structural analysis of human and murine flt3 l; A; Reference number: 139075; MUID:96032581; PMID:7566977
A; Accession: 149347
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Moccule type: DNA
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Moccule type: DNA
A; Translated from GB/EMBL/DBBJ
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A;Reference number: S43290; MUID:94195428; PMID:8145851
A;Accession: S43290
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-197,'L',198-231 <RE2>
A;Residues: 1-197,'L',198-231 <RE2>
A;Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90951.1; PID:g1072040
R;Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazz
felt, A.; Muench, M.; Kelner, G.; Namikawa, R.; Rennick, D.; Ronçarolo, M.G.;
Mature 368, 643-648, 1994
           Qγ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-197, 'L', 198-231 <HAN>
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
C;Accession: A49265; I49347; I49346; S43290
R;Lyman, S.D.; James, L.; Vanden Bos, T.; de Vries, P.; Brasel, K.; Gliniak, D.; Williams, D.E.; Beckmann, M.P.
Cell 75, 1157-1167, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Note: the sequence from Fig. 2c is inconsistent with
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A;Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90952.1; PID:g1072041
A;Accession: I49346
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A;Accession: A49265
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A; Residues: 1-231 <LYM>
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flt3/flk-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                  LRFVQTNISRLLQETSEQLVALKPWITR--QNFSRCLELQCQPDSSTLPPPWSPRPLEAT 177
APTAPQPP--LLLLLLLPVGLLLLAAAWCLHWQRTRRTPRPGEQVPPVPSP 227
                                                                                                                                                                                                                                                  VASNIQDEELCGGIJWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC 119
                                                                     LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
                                                                                                                                                                                                                 VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                                                                                                                                                                          MTVLAPAWSPNSSILLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ligand precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.9%;
70.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 768.5; DB:
Pred. No. 1.8e-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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urawski, S.; Bazan, J.F.; Ronçarolo, M.G.; Zlotnik

Fig.

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having

9:

Gaps

4;

180

120

PID: 9439442

Escobar,

S

K.; Gliniak,

B.; Holl

receptor:

201

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PLT3/FLK2 ligand (clone T118) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C;Accession: S43291
R;Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, felt, A.; Muench, M.; Kelner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zl
Nature 368, 643-648, 1994
A;Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haema A;Reference number: S43290; MUID:94195428; PMID:8145851
A;Accession: S43291
A;Molecule type: mRNA
A;Residues: 1-220 <HANN
                                                                                                                                                                                                                                                                                                                                                                 flt3 ligand isoform 5H - mouse C;Species: Mus sp. (mouse) C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999 C;Accession: I58343 R;Lyman, S.D.; James, L.; Escobar, S.; Downey, H.; de Vries, P.; Brasel, K.; Oncogene 10, 149-157, 1995 A;Title: Identification of soluble and membrane-bound isoforms of the murine A;Reference number: I58343; MUID:95124710; pMID:7824267 A;Accession: I58343
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A;Cross-references: GB:S76459; NID:g913479; PIDN:AAB33069.1; PID:g913480
                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-220 < RES>
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Best Local Similarity
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Best Local
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 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LREVQTNISRLLQETSEQLVALKPWITR--QNFSRCLELQCQPDSSTLPPPWSPRP---- 173
                                                                                                                                                                  MTVLAPAMSP-TTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATRUTATALLTVCPGLLLPLVGTSHMFFLPYFLSFLSS 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRFVQTNISRLLQETSEQLVALKPWITR--QNFSRCLELQCQPDSSTLPPPWSPRP---- 173
                                                                                                          VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VASNIQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC 119
LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPGNG---
                                                                     VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC 120
                                                                                                                                               MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT 60
                                                                                                                                                                                                                        134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---LEATAPTAPQPPLLL-----LLLLPVGLLLLAA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPGNG-----GPRAQHHG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT 60
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                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                       48.8%;
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                                                                                                                                                                                                                      18;
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; Pred. No. 1.3e-44;
18; Mismatches 43
                                                                                                                                                                                                                                       Score 606.5;
Pred. No. 1.3
                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                       .3e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                      43; Indels
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                                                                                                                                                                                                                                                         Length 220;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             P.; Brasel, K.; Stocking,
GPRAQHHG
                                                                                                                                                                                                                      23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23;
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R; Barlow, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-1217 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A; Accession: T22672
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                                                                                                                                                                                                                                                                            C; Genetics:
                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-661 <DAV>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: CESP:F54F12.1
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Best Local
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                                                                                                                                                Matches
                                                                                                            19
                                  72
                                                                       79
                                                                                                                                                              Local Similarity
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C;Accession: C27342

R;Davison, A.J.; Scott, J.E.
J. Gen. Virol. 67, 1759-1816, 1986
A;Title: The complete DNA sequence of varicella-zoster A;Reference number: A27345; MUID:86306657; PMID:3018124
A;Accession: C27342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F54F12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNBE12
74K alpha trans-inducing protein - human herpesvirus 3
74K alpha trans-inducing protein - human herpesvirus 3
C:Species: human herpesvirus 3, varicella-zoster virus
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                       A;Gene: 12
C;Superfamily: herpesvirus 77K alpha trans-inducing protein
C;Keywords: trans-inducing protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, A; Reference number: Z19597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: clone C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: EMBL: X04370; NID: g59989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:Z81548; NID:e1062020; PIDN:CAB04464.1; GSPDB:GN00021; CESP:FA;Experimental source: clone F54F12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       743 GAVGGLLVVAIIGVILFFVFFQKKKKKEDKPDD--PPAPLP 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPVGLLLLAA-----AWCLHWQRTRRRTPRPGEQVPPVPSP 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATRITATALLTVCPGLLLPLVGTSHMFFLPYFLSFLSS
                                                                                                                                                                      LLSSGLSGTQDCS----FQHSPISSDFAVKI--RELSDYLLQDYPVTVASNLQDEELCG- 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALKPWITRQNFSRCLELQCQPDSSTL---PPPWSPRPLEATAPTAP-----QPPLLLLLL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MERLKTVAGSKMQGL---LERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLV 139
GLW-WVYENTYWQYLKYTTGAEVPVTSEKVNKKSKSTVLLFSSVVANKPISRHPFKSKVI
                                                   GLWRLVLAQRWMERLKTVAGSKMQGLLERVN----TEIHFVTKCAFQP---PPSCLRFV 123
                                                                                                                LTSPVLQSTERHSVLLGLHHNNVPESLVVSCMSNDVHDGFMQRYMETIQRCLDDLKLSGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALRPOPTTSDPTAAAPVPIPNNKGSLNGNPSPSSPPLLPPVASSTPAATPEESNMLLYII 742
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                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       884/2; 922/3; 972/1; 1024/2;
                                                                                                                                                                                                                                                     7.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33;
                                                                                                                                                                                                                                   29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 93; DB 2
Pred. No. 8;
33; Mismatches
                                                                                                                                                                                                                                                     Score 92;
Pred. No. '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from
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                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                   DB 1; Length 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIDN:CAA27895.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 1217;
                                                                                                                                                                                                                                103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                PID:960001
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                                                                                                                                                                                                                             Gaps
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                                                                                                                138
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A;Title: Adhalin mRNA and cDNA sequence are normal in the cardiomyopathic | A;Reference number: I48201; MUID:95278335; PMID:7758576
A;Accession: I48201
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: I-387 <RESA
A;Cross-references: EMBL:U21677; NID:9726481; PIDN:AAA81645.1; PID:9726482
C;Superfamily: mouse adhalin
                                                                                                                                                                                                                                                           adhalin - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Jun-2000
C;Accession: I48201
R;Roberds, S.L.; Campbell, K.P.
FEBS Lett. 364, 245-249, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein C28D4.2 - Caenorhabditis elegans (;Species: Caenorhabditls elegans C;Species: Caenorhabditls elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T19543 R;McMurray, A. submitted to the EMBL Data Library, November 1996 A;Reference number: Z19139 A;Accession: T19543 A;Accession: T19543 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Mclocule type. DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qγ
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A:Introns: 26/3; 72/3; 118/2; 169/1; 203/2; 240/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       БР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: CESP: C28D4.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-474 <WIL>
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.2%; Score 89.5; DI Best Local Similarity 24.1%; Pred. No. 5.5; Matches 59; Conservative 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267 ITVAQ 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 LLLVE 234
                                                                                                                                                                                                                                                                                                                                                                                                                             10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 GYGWMLWFLDVVD-----ARVCRHLKLQFRRIRGPRASV----IPDDLL 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 VLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLR-FVQTNISRLLQET- 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PKEPQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTAPQPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTP---RPGE-----QVPPVPSPQD 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VFTLLSERNLGPKMLGVFPGGRFEQFIPSRALQCLEISKPGLSKLIAPIVARVHTLDAPI 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TQDC-----SFQHS-PISSDFAVKIREL-SDYLLQDYPVTVASNLQDEELCGGLWRL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QPPLLLLLLPVGLLLLAAAWCLHWQRTRRTPRPGEQVPPVPSPQDLL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----SEQLVALKPWITRQNFSRCLELQC----QPDSSTLPPPWSPR--PLEATA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VKIEEF--RIRAITGG-MSNLLFLVELPAH-LTPIQMEPEKALLRVHCQSDIDQLLSESV 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NSDYRGICQELREALGAVQKYM---YFMR------PDDPTNPSPDTRIRVQETAAYTAT 247
       7.2%;
23.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -TLQTARQWLERF----KKTPAGERPIEMYLTQAKVPKSDYPST 266
       Score 89; DB 2; Pred. No. 4.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262/3; 298/3; 342/2; 391/3
                            Length 387;
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                                                                                                                                                                                                                                    cardiomyopathic hamster
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	Oy 146TRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT 180   :  :  :
	QY 108 VTKCAFQPPDSCLRF
	QY 64 LQDEELCGGLWRLVLAQRWME-RLKTVAGSKMQGLLERVNTEIHF 107
i	QY 4 LAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASN 63
17;	Query Match 7.2%; Score 89; DB 1; Length 793; Best Local Similarity 22.3%; Pred. No. 11; Matches 67; Conservative 34; Mismatches 79; Indels 120; Gaps
ĭ	A;Gene: GDB:SF3A120; PRP21; SAP114 A;Gene: GDB:SF3A120; PRP21; SAP114 A;Cross-references: GDB:9955873 A;Map position: 22q12.1-22qter C;Superfamily: human splicing factor SF3a 120K chain; ubiquitin homology C;Keywords: pre-mRNA splicing F;714-790/Domain: ubiquitin homology <ubh></ubh>
	A; Molecule type: protein A; Molecule type: protein A; Residues: 51-62; 82-94; 270-275; 397-414; 448-463 < KRA2> C:Genetics:
	A;Status: nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 1-793 <kra> A;Cross-references: EMBL:X85237; NID:g899297; PIDN:CAA59494.1; PID:g899298 A:ACCession: 66723</kra>
SURP family	oresents a new member of the
•	<pre>splicing factor SF3a 120K chain - human C;Species: Homo sapiens (man) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000 C;Accession: S60735; S60733 R;Kraemer, A.; Mulhauser, F.; Wersig, C.; Groening, K.; Bilbe, G.</pre>
	RESULT 11 S60735
	Db 384 LDQH 387
	324 MATSE
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
	QY 162 SSTLPPPWSPRPLEATAPTAPQPPLLLLLLPVGLLLLAAAWC 204  :
	Qy 111 CAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWITRQNESRCLELQCQPD 161
	Qy 71 GGLWRLK 110
	QY 11 TTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELC 70
14;	Matches 71; Conservative 26; Mismatches 97; Indels 110; Ga

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DNA Res. 4, 345-349, 1997
A;Title: Characterization of cDNA clones in size-fractionated cDNA libraries from human A;Reference number: Z14085; MUID:98116662; PMID:9455484
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T00257
    DЬ
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                                                                                                                                                                                                                                   A:Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNAA;Residues: 1-1386 <SEK>
                                                                                                                                                                                                                                                                                                                                                   R;Seki, N.; Ohira, M.; Nagase,
DNA Res. 4, 345-349, 1997
                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C;Accession: T00257
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A;Residues: 1-238 <KUR>
A;Cross references: GB:BA0000019; PIDN:BAB77837.1;
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C;Accession: AB1990
                                                                                                                                                            A; Note:
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                                                                                                                                                                                             A; Experimental source:
                                                                                                                                                                                                                 A;Cross-references: EMBL:AB007945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein KIAA0476 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: AB1807; A; Accession: AB1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein all1471 [imported] - Nostoc sp. C:Species: Nostoc sp.
                                                                               Matches
                                                                                                                   Query Match
                                                                                                                                                                                Genetics
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Best Local Similarity
    1104
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                                        21
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                                                                                                                                                          KIAA0476
    SAGASGSKDAPVPGGP
                                    SSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELC----GGLWRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVALKPWITRQNFSRCLELQCQPDSSTLPPPW---SPRPLEATAPTAPQPPLLLLLLLPV 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSPISSDFAVKIRELSDYLLQDY---PVTVASNLQDEELCGGLWRLVLAQRWMERLKTVA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MPRPPMASVVRLPPGSVIAPMPPIIHAPRINVVPMPPSAPPIMAPRPPPMIVPTAFVPAP 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APQPPLLLLLLLPVGLLLLAAAWCLHWQRTR-----RRTPRPGEQVPP---VPSP 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PQSLKP--TKPIPPKLIEPKKSEDSKNLQRPRIPDSPKPIKNSQPEAPKPV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSKKTTTYYESINEVCNQYLKSYEKKPLVII-----QILG--W----SQRLMRYYKTVD 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44;
                                                                           . Similarity 23.: 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.; Shimpo, S.
205-213, 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.1%;
                                                                                                 7.1%;
23.1%;
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                                                                                                                                                                                                                                                                                                                                                                   T.;
                                                                             28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 88.5; D; Pred. No. 3; 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32;
                                                                           Score 88.5; I
Pred. No. 23;
28; Mismatches
                                                                                                                                                                                                             NID:g3413913; PIDN:BAA32321.1; PID:g3413914
                                                                                                                                                                                                                                                                                                                                                             Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura,
-GPVLSDRRLCLA--LDEPQLCNGHMGGASRR 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -VVRKIPKVIETPKIVKPQKTEDIKTLES 174
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                                                                                                                   DΒ
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                                                                                                               Length
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                                                                             Indels
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                                                                         63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Watanabe, A.; Iriguch:
Yasuda, M.; Tabata, S
                                                                         Gaps
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A; Title: Complementation of fission yeast cdc2(ts) and A; Reference number: S12008; MUID:91006056; PMID:2120044
                                                                                                                                                                                                                                            A; Title: Genetic control of cell division patterns in the A; Reference number: A32290; MUID:89195217; PMID:2702688 A; Accession: A32290
                                                                                                                                                                                                                                                                                                               R;Edgar, B.A.; O'Farrell, P.H.
Cell 57, 177-187, 1989
                                                                                                                                                                                                                                                                                                                                                         protein-tyrosine-phosphatase (EC 3.1.3.48) cdc25 homolog string - fruit fly (Drosophi
C;Species: Drosophila melanogaster
C;Date: 05-Oct-1989 #sequence_revision 25-Apr-1997 #text_change 11-Jun-1999
C;Accession: A32290; S12008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Ding, S.; Keese, P.; Gibbs, A.
J. Gen. Virol. 71, 925-931, 1990
A;Title: The nucleotide sequence of the genomic RNA of A;Reference number: JQ0532; MUID:90218040; PMID:2324710
A;Accession: JQ0532
A; Residues: 1-227, 'A', 229-479 <JIM>
A; Cross-references: EMBL:X57495; NID:g7706; PIDN:CAA40732.1;
                         A; Molecule type: mRNA
A; Residues: 1-227, 'A', 229-479
                                                                A; Accession: S12008
                                                                                                                                    R; Jimenez, J.; Alphey, L.; EMBO J. 9, 3565-3571, 1990
                                                                                                                                                         A;Cross-references: GB:M24909; NID:g158507; PIDN:AAA28916.1; R;Jimenez, J.; Alphey, L.; Nurse, P.; Glover, D.M.
                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-479 <EDG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OP protein - Kennedya yellow mosaic virus
C:Species: Kennedya yellow mosaic virus
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qy
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A; Residues: 1-753 <DIN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               534 PPDVFHDCQPSSPTSHVVGYRRLLGSGISLPFKLAFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           420 RLSTQPPSSPQTSSSPPPPSPRTDASGIQTPLASPPSKRKEKSLPHPSHQ----PPSHSK 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 QNFSR----CLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 RVNTEIHFVTKCAFQPPPSCLRF----VQTNIS-----RLLQETSEQLVALKPWITR 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 LLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VESGAWAYLSPLVLRKELESLVENEGSEV-----LALPELPSAHPIIFWNLLWYFQRL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 88; DE Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -VGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58;
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                                                                                                               cdc25(ts) mutants identifies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                           PID:g158508
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PID: 97707

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8, 8
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A;Gene: FlyBase:stg
A;Gene: FlyBase:stg
A;Cross-references: FlyBase:FBgn0003525
C;Function:
A;Description: catalyzes hydrolysis of peptidyl-phosphotyrosine to peptidyl-tyrosine and A;Description: catalyzes hydrolysis of peptidyl-phosphotyrosine to peptidyl-tyrosine and A;Pathway: initiation of mitosis
A;Note: cdc25 activates the cdc2 protein kinase by dephosphorylating it
C;Superfamily: protein-tyrosine-phosphatase string; cdc25-type protein-tyrosine-phosphatase:
C;Keywords: cell cycle control; mitosis; phosphoprotein; phosphoric monoester hydrolase;
F;352-456/Domain: cdc25-type protein-tyrosine-phosphatase homology <PTP>
F;379/Active site: Cys (phosphocysteine intermediate) #status predicted
F;385/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                        ·В
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                                                                                                                                                                           Qy
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Search completed: November 24, 2002, 10:12:12 Job time : 17.6245 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 7.0%; Score 87.5; DI Best Local Similarity 22.9%; Pred. No. 8.2; Matches 56; Conservative 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 118 SCLRFVQTNISRLLQETSBQLVALKP---WITRQNFSRCLEL-QCQPDSSTLPPPWSPRP 173
                                                                                                                     243 VTISH 247
                                                                                                                                                                                  231 LLVEH 235
                                                                                                                                                                                                                                           200 ---TARDCFKRPEPP----
                                                                                                                                                                                                                                                                                                 174 LEATAPTA---POPPLILLILLEVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDL 230
                                                                                                                                                                                                                                                                                                                                                                 147 SGLN-----SLISGQIKEQPAAKSPAGLSMRRPSVRRCLSMTESNTNSTTTPPPKTPE- 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 CSMESSMDDE-----P 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 VTVASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPP 117 : | : | : | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 MGLLSPEGSPQRFQIVRQPKILPAMGVSS------DHTPARS-FRI-FNSLSS-----T 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MTVLAPAWSPTTYLLL---LLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYP 57
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

ယ္	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	<sub>5</sub>	4	ω	2	Ľ	Result
80	80	80	80	80.5	81	81	81	81	81.5	Ľ	81.5	82	83	83.5	84	84	84	84.5	85	85		86.5	87	8	87.5		89	89	89.5	92	768	1242	Score
6.4	6.4	6.4	6.4						٠					٠		6.8	•				6.9	7.0	7.0	7.0	7.0	7.0	7.2	7.2	7.2	•	61.8	100.0	Query Match
1794	1174	940	397	1402	1248	428	387	283	2124	591	488	2167	758	671	1234	732	582	3726	366	282	485	1394	911	910	479	415	793	387	941	661	232	235	Length [
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YAV1_SCHPO	KPC1_COCHE	GBR2_RAT	CEFD_STRCL	IF4G_RABIT	DIA1_HUMAN	EPC_HUMAN	SGCA_MOUSE	ATF5_MOUSE	Y192_HUMAN	MNT_MOUSE	MM11_HUMAN	SHK1_RAT	VKGC_HUMAN	Z282_HUMAN	NPHN_RAT	YF48_HUMAN	MNT_HUMAN	ABF1_MOUSE	FCGN_RAT	ATF5_HUMAN	SSGP_VOLCA	CNG4_BOVIN	DDR1_MOUSE	ı	MPIP_DROME	TNR3_MOUSE	S3A1_HUMAN	SGCA_MESAU	GBR2_HUMAN	ATI2_VZVD	FL3L_MOUSE	FL3L_HUMAN	ID
Q10172 schizosacch	$\sim$		ø	oryc	homo	homo		mus m	Q93074 homo sapien	9 mus n	hom		homo	Q9udv7 homo sapien	rattu	4 homo	homo	Q61329 mus musculu		Q9y2d1 homo sapien		sod				4 mus m	Ø	5 mesoc	075899 homo sapien	**	P49772 mus musculu		Description

45	44	43	42	41	40	39	38	37	36	35	34
77	77.5	77.5	77.5	78	78	78.5	78.5	78.5	78.5	78.5	79
6.2	6.2	6.2	6.2	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.4
195	2004	1885	341	566	205	1180	913	387	382	251	805
Н	ш	1	1	ш	ب	Н		Н	ш	ب	ب
CORA_HPBVF	MOZ_HUMAN	FAS2_CANAL	PLSX_VIBCH	TS13_MOUSE	CYSR_SYNY3	ATY1_HUMAN	DDR1_HUMAN	SGCA_RABIT	AVRB_RAT	HXB4_HUMAN	YGW6_YEAST
						Q9nq11				-	P53086
hepatitis b	homo sapien	c fatty aci	vibrio chol	mus musculu	synechocyst	homo sapien	h epithelia	oryctolagus	rattus norv	homo sapien	saccharomyc

## ALIGNMENTS

6666666687	RA R	R R R R R R R R R R R R R R R R R R R	FL3L_H FL3L_H ID E AC P. DT 0 DT 1 DE 1. DE 1. DE S. OC E OC M
Dundles and cystine knots";  Nat. Struct. Biol. 7:486-491(2000).  -i- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING FACTORS AND INTERLEUKINSi- SUBUNIT: Homodimer (isoform 2)i- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1); secreted (isoform 2)i- ALTERNATIVE PRODUCTS: 2 isoforms; a l/membrane-bound (shown here) and 2/soluble; are produced by alternative splicing.		SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  MEDLINE=94195428; PubMed=8145851; Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S., Hannum C., Culpepper J., Hudak S., Wagner J., Mattson J., Luh J., Bazan J.F., Kastelein R., Hudak S., Wagner J., Mattson J., Luh J., Duda G., Martina N., Peterson D., Menon S., Shanafelt A., Muench M., Kelner G., Namikawa R., Rennick D., Roncarolo M.G., Zlotnik A., Rosnet O., Dubreuil P., Birnbaum D., Lee F.; "Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoletic stem cells and is encoded by variant RNAs."; Nature 368:643-648(1994).  [2] Nature 368:643-648(1994).  [2] SEQUENCE FROM N.A. MEDLINE=94235842; PubMed=8180375; Lyman S.D., James L., Johnson L., Brasel K., de Vries P., Escobar S.S., Downey H., Splett R.R., Beckmann M.P., McKenna H.J.; "Cloning of the human homologue of the murine flt3 ligand: a growth factor for early hematopoletic progenitor cells."; Blood 83:2795-2801(1994).	FESULT 1  FESULT 1  ID FLSIL_HUMAN STANDARD; PRT; 235 AA.  AC 949771; DT 01-CCT-1996 (Rel. 34, Created) DT 01-CCT-1996 (Rel. 34, Last sequence update) DT 15-JUN-2002 (Rel. 41, Last annotation update) DE SL cytokine precursor (Fms-related tyrosine kinase 3 ligand) (Flt3) DE 11gand) (Flt3L). GN FLT3LG. OS Homo sapiens (Human). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.  OX NCBL_TaxID=9606;

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RESULT 2
F131_MOUSE
ID F131_M
AC P49772
DT 01-OCT
DT 15-JUN
DE SL Cyt
LE 11gand
GN F173LG
OS MUS mU
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Best Local
                                                                              FL3L_MOUSE STANDARD: PRT; 232 AA.
P49772; Q64085;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
SL cytokine precursor (Fms-related tyrosine Kinase ligand) (F151).
FLT3LG OR FLT3L.
SEQUENCE FROM N.A.
MEDLINE=94195428; PubMed=8145851;
                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARSPLIC CONFLICT
                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
VARSPLIC
                                    NCBI_TaxID=10090
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EMBL; U03858; AAA19825.1; --
EMBL; U29874; AAA90949.1; --
EMBL; U29874; AAA90950.1; --
PDB; LETE; 09-JUN-00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                      APQPPLLLLLLPVGLLLLAAAMCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH
                                                                                                                                                                                                                                                                        REVQTNISRLLQETSEQLVALKPWITRQNESRCLELQCQPDSSTLPPPWSPRPLEATAPT
                                                                                                                                                                                                                                                                                      RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT
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Rodentia;
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SL CYTOKINE.
EXPRACELULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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N-LINKED (GLCNAC. ..) (POTENTIAL).
DSSTLPPPWSPRPLEATA -> VETVFHRVSQDGLDLLTS
                                           Craniata; Ver
Sciurognathi;
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Pred. No. 1.1e-96;
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thi; Muridae;
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EMBL; U04807; AAA18000.1; -
EMBL; L23636; AAA39436.1; -
EMBL; U29875; AAA90951.1; -
EMBL; U29875; AAA90952.1; -
EMBL; S76459; AAB33069.1; -
EMBL; S76464; AAB33070.1; -
EMBL; S76464; AAB3307.1; -
EMBL; U44024; AAA93307.1; -
EMBL; U44024; AAA93306.1; -
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                               InterPro; IPR004213;
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                                                                                                                                                                                                                                                                                                   use
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                                                                                                                                                                                                                                                                                                              the European
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Lyman S.D., James L., Vandenbos T., Devries P., Brasel K.,
Gliniak B., Hollingsworth L.T., Picha K.S., McKenna H.J.,
Splett R.R., Fletcher F.A., Maraskovsky E., Farrah T.,
Foxworthe D., Williams D.E., Beckmann M.P.;
"Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase
receptor: a proliferative factor for primitive hematopoietic cells.";
C211 75:1157-1167(1993).
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McClanahan T., Cul
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Brasel K., Stocking K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Structural analysis of human and murine flt3 ligand genomic loci."; oncogene 11:1165-1172(1995).
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SUBGURIT: Homodimer (soluble isoform) (By similarity).
SUBCELLULAR LOCATION: Type I membrane protein. Two sol isoforms are also produced by alternative splicing. On isoform 3/E6, is biologically active, while the other, 4/E6Delta16, is inactive.
ALTERNATIVE PRODUCTS: 4 isoforms; 1/6C (shown here), 2 and 4/E6Delta15; are produced by alternative splicing.
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                                               MGI:95560;
                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way by non-profit.
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                                               Flt31.
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                                                              .......
                                                                                                                                                                                                                                                   is not removed. Usage by and for commercial agreement (See http://www.isb-sib.ch/announce/
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N.G.,
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Glycoprotein;

Transmembrane; Alternative splicing; Signal.

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RESULT 3
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       the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-NOV-1990
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                                                                                                                                                                                                                              Varicella-zoster virus
                                                                                                                                                                                                                                                      Alpha
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                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=86306657; PubMed=3018124;
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AR-1989 (Rel. 10,
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a trans-inducing :
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                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                         complete DNA sequence of varicella-zoster virus.";
en. Virol. 67:1759-1816(1986).
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MISSING (IN REF. 2).
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                                                                                                                                                                                                                                                                                                              PRT;
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Gamma-aminobutyric acid type B receptor, subunit 2 precursor (GABA-B receptor 2) (GABA-B-R2) (GBABA-B) (GABABR2) (G protein-coupled receptor 51) (GPR 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN
                                                                                                                                                                                                                                             Herzog H.; "Cloning and characterization of a novel human "Cloning and characterization of a novel human with high affinity for GABA and low affinity fo submitted (NOV-1998) to the EMBL/GenBank/DDBJ of the EMBL/GenBank/DD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IR005051; Herpes_U146.
Pfam; PF03387; Herpes_U146; 1.
Transcription regulation; Trans-a
SEQUENCE 661 AA; 74272 MW; C5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clark J.A., Mezey E., Lam A.S., Bonner "Distribution of the GABA(B) receptor Brain Res. 860:41-52(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        White J.H., Wise A., Main M.J., Green A., Fraser N.J., Disney G.H. Barnes A.A., Emson P., Foord S.M., Marshall F.H.; "Heterodimerization is required for the formation of a functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 2A)
TISSUE=Cerebellum;
MEDLINE=99087321; PubMed=987231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GBR2_HUMAN
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                                                                      Borowsky B., Laz T.,
Submitted (JAN-1999)
                                                                                                                  SEQUENCE FROM N.A. TISSUE-Hippocampus;
Borowsky B., Laz T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Heterodimerization is required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20193514; PubMed=10727622;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parker R.,
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(ISOFORM
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                                                                                                                                                                                                                                                                                                                                                                                                                    M 2A).
K., Watson
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2A)
                                                                               C.;
EMBL/GenBank/DDBJ
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            J.,
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a collaboration

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AL J. Pharmacol. Exp. Ther. 293:460-467(2000).

1. PHORTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS C. -! FUNCTION: RECEPTOR FOR FAMELS.

2. MEDIATED BY G-PROTEINS THAT INHIBITS ADENTIFY CYCLASE ACTIVITY, CYCLASE AC
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"Coexpression of full-length gamma-aminobutyric Acid(B) (GABA(B)) receptors with truncated receptors and metabotropic glutamate receptor 4 supports the GABA(B) heterodimer as the functional
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J. Biol. Chem. 274:7607-7610(1999).
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Ng G.Y.K., Clark J., Coulombe N., Ethier N., Hebert T.E., Sullivan Kargman S., Chateauneuf A., Tsukamoto N., McDonald T., Whiting P., Mezey E., Johnson M.P., Liu Q., Kolakowski L.F. Jr., Evans J.F.,
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"Molecular identification of the human GABABR2:
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Ng G.Y.K., McDonald T., Bonnert T., Rigby M., Heavens R., Whiting Chateauneuf A., Coulombe N., Kargman S., Caskey T., Evans J.F.,
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MEDLINE=99189236; Pu
Ng G.Y.K., McDonald
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                                  TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN, ESPECIALLY IN CEREBRAL CORTEX, THALAMUS, HIPPOCAMPUS, FRONTAL, OCCIPITAL AND TEMPORAL LOBE, OCCIPITAL POLE AND CEREBELLUM, FOLLOWED BY CORPUS CALLOSUM, CAUDATE NUCLEUS, SPINAL CORD, ANYGDALA AND MEDULLA. WEAKLY EXPRESSED IN HEART, TESTIS AND SKELETAL MUSCLE. DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION MEDILATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 1.

SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                    HAPPEN.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MO
COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO
PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B
PLASMA MEMBRANE.

ALTERNATIVE PRODUCTS: 3 ISOFORMS; 2a (SHOWN HERE),
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TISSUE SPECIFICITY: HTOHY TOTAL
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SUBUNIT: HETERODIMER
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                          RECEPTOR
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Pfam; PF01094; ANF_receptor; 1.

PFAM; PF01094; ANF_receptor; 1.

PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; FALSE_NEG.

PROSITE; PS00980; G_PROTEIN_RECEP_F3_3; FALSE_NEG.
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InterPro; IPR000337; GPCR_Mgr.
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L; AF095723; AAC6328.1;
L; AF095724; AAC63383.1;
L; AF095724; AAC63384.1;
L; AF095784; AAD30384.1;
L; AF095784; AAD30336.1;
L; AF094785; AAC99345.1;
L; AF069755; AAC99345.1;
L; AF0699033; AAD45867.1;
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Sakamoto A., Ono K., Abe M., Jasmin G., Eki T., Murakami Y.,
Masaki T., Toyo-oka T., Hanaoka F.;
"Both hypertrophic and dilated cardiomyopathies are caused by mut
of the same gene, delta-sarcoglycan, in hamster: an animal model
disrupted dystrophin-associated glycoprotein complex.";
proc. Natl. Acad. Sci. U.S.A. 94:13873-13878(1997).
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Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vert
Mammalia; Eutheria; Rodentia; Sciurognathi;
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16-ocr 2001 (Rel. 40, Last sequence update)
15-JUN 2002 (Rel. 41, Last annotation update)
Alpha-sarcoglycan precursor (Alpha-SG) (Adhal
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RA Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beasley O.P.,
Balley J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bagguley C., Balley J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Brid C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
Clark G., Collier R.E., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
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RA Clegg S.M., Cobley V.E., Coville G.J., Cox A.V., Davis J., Davson E.,
RA Glibert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcott R.M., King A.,
RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Mashreghi Mohammadi M., Matthews L.H., Mccann O.T.,
RA McClay J., Mclaren S., McMurray A.A., Milne S.A., Mortinore B.J.,
RA McClay J., Mclaren S., McMurray A.A., Milne S.A., Mortinore B.J.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
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RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Phan S., Gis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Wang Q., Wang Y., Wang Z., White J., Williangham D., Wu H., Yao Z.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96079958; PubMed=7489498;
Kraemer A., Mulhauser F., Wersig C., Groning K
Traemer A., Mulhauser F., Wersig C., Groning K
"Mammalian splicing factor SF3a120 represents
SURP family of proteins and is homologous to t
factor PRP21p of Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Splicing factor 3 subunit 1 (Spliceosome associated protein 114) (SAP
114) (SF3a120):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S3A1_HUMAN
Q15459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20057165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SF3A1 OR SAP114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MATSDIQMVHHCTIHGNTEELRQMAARREVPRPLSTLPMFNVRTGERLPPRVDSAQVPLI 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSTLPPPWSPRPLEAT-----APTAPQPPLLLLLLLPVGLLLLAAAWC------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=10591208;
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FINITIONAL ASSOCIATION OF U2 SNRNP WITH THE ATP-INDEPENDENT ENDITIONS SUBUNITY OF THE SPLICING FACTOR SF3A REQUIRED FOR 'A'
CC --- FUNCTION: SUBUNITY OF THE SPLICING FACTOR SF3A REQUIRED FOR 'A'
CC COMPLEX ASSEMBLY FORMED BY THE STABLE BINDING OF U2 SNRNP TO THE BRANCHPOINT SEQUENCE (BPS) IN PRE-MRNA. SEQUENCE INDEPENDENT
CC BINDING OF SF3A/SF3B COMPLEX UPSTREAM OF THE BRANCH SITE IS
ESSENTIAL, IT MAY ANCHOR U2 SNRNP TO THE PRE-MRNA. MAY ALSO BE
CC INVOLVED IN THE ASSEMBLY OF THE 'E' COMPLEX.
CC --- SUBUNIT: COMPONENT OF SPLICING FACTOR SF3A WHICH IS COMPOSED OF THREE SUBUNITS: SF3A3/SAP61, SF3A2/SAP62, SF3A1/SAP114. SF3A
CC ASSOCIATES WITH THE SPLICING FACTOR SF3B AND A 12S RNA UNIT TO FORM THE U2 SMALL NUCLEAR RIBONUCLEOPROTEINS COMPLEX (U2 SNRNP).
CC --- TISSUE SPECIFICITY: UBICULTOUSLY EXPRESSED.
CC --- SUBULLARITY: TO YEAST PRE-MRNA SPLICING FACTOR PRE21.
CC --- SIMILARITY: TO YEAST PRE-MRNA SPLICING FACTOR PRE21.
  Matches
                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P., Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S., Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J., Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T., Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J., Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L., Kim U.J., Shizuya H., Sinon M.I., Dumanski J.P., Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan, S., Taliahum V., P., Bodenteich A., Hartman K., Hu X., Khan, S., Taliahum V., P., Bodenteich A., Hartman K., Hu X., Khan, S., Taliahum V., Pariahum V., Pariah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tilahun Y., Wright H.;
"The DNA sequence of human chromosome 22.";
Nature 402:489-495(1999).
                                                                                                                                                                DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHARACTERIZATION OF THE SPLICEOSOME.
                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000061; Surp.
InterPro; IPR000626; Ubiquitin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                            SEQUENCE
                                                                                                                  DOMAIN
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                                                                                                                                                                                                                                                                                  REPEAT
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                                                                                                                                                                                                                                                                                                            REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                       PF00240; ubiquitin;
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  1 Similarity 67; Conser
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                                                                                                                                                                                                                                                                                                                                                                              SM00213; UBQ;
                                                                                         52
166
107
10
118
118
260
369
557
672
793 AA;
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC23435.1;
                                                                                                                                                                                                                                                                                                                                                   UBIQUITIN_2; 1
                                                                                                                                                                                                                                                                                                                                processing;
                                                                                                                                          208
793
16
122
122
267
372
560
                     7.2%;
                                                                                              WW.
  34;
Score 89; DB
Pred. No. 5.8;
34; Mismatches
                                                                                                                                                           UBIQUITIN-LIKE.
POLY-PRO.
POLY-GLN.
POLY-GLU.
POLY-PRO.
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                                                                                                                                                                                                                                                                                                                             mRNA splicing;
                                                                                              7259F1EC4577305C CRC64
                                              1;
                                                                                                                                                                                                                                                                                                                                Nuclear protein; Repeat.
  79;
                                              Length 793;
  Indels 120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a collaboration
  Gaps
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    17;
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Qγ

4 LAPAWSPTTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASN 63

MGD; MGI:104875; Lt.br

IPR001368;

TNFR\_c6

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TNR3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The murine lymphotoxin-beta receptor cDNA: isolation sequence trap and chromosomal mapping."; Genomics 30:312-319(195).

-!- FUNCTION: Receptor for the heterotrimeric lymphoto
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
EMBL; U29173; AAA68964.1; -.
EMBL; L38423; AAB00846.1; -.
EMBL; U30798; AAA81334.1; -.
HSSP; O14763; LDOG
                                                                                                                                 or send an
                                                                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Honjo T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=96163885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Browning J.L., Ware C.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96072804; FubMed=7594541; Force W.R., Walter B.N., Hession
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STRAIN=CVB; TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LTBR OR TNFRSF3 OR TNFCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNR3_MOUSE
                                                                                                                                                               entities requires
                                                                                                                                                                                                                                                                        between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakamura T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                               SUBUNIT: Self-associates (By similarity)
SUBCELLULAR LOCATION: Type I membrane pr
SIMILARITY: CONTAINS 4 THER-CYS REPEARS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MPRPPMASVVRLPFGSVIAPMPPIIHAPRINVVPMPPSAPPIMAPRPPPMIVPTAFVPAP 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEETAIGKKIGEEEIQKPEEKVTWDGHSGSMARTQQAAQANIT--LQEQIEAIHKAKGLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MQEHMRIG-----ILDPRWLEQRDRSIREKQSDDEVYAPGLDIESSLKQLAER-RTDIFG
                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                            and TRAF5. May play a role in (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LQDEELCGGLWRLVLAQRWME-RLKTV------
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                                                                                                                                    email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   155:5280-5288(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tashiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor for the heterotrimeric lymphotoxin containing TB, and for TNFS14/LIGHT. Promotes apoptosis via TRAF3 May play a role in the development of lymphoid organs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=8586432;
                                                                                                                                                               tatement is not removed. Usage by and for commercial
license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K., Nazarea M., Nakano T., Sasayama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hession C., Tizard R., Kozak C.A.,
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|------SPITGE---KI--
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Best Local
                                                                                                                                                                                                                                                                                                                         MPIP_DROME STANDARD; r...,
MPIP_DROME STANDARD; 
                                                                                                                                                                                   urosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
             MEDLINE-91006056; PubMed-2120044; Jimenez J., Alphey L., Nirror
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protein).
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TRANSMEM
                                                                                                         Edgar B.A., O'Farrell P.H.;
"Genetic control of cell division patterns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00020; TNFR_C6; 3.
ProDom; PD000771; TNFR_C6; 1.
SMART; SM00208; TNFR; 3.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 3.
     "Complementation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236
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                                                                                            57:177-187(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FTTVLACAWMRHPSLCRKLGTLLKRHPE-GEESPPCPAPR 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----LAAAWCLHWQRTR-----RRTPRPGEQVPPVPSPQ 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ECRCQPGMSCVYLDNECVHCEEERLVLCQPGTEAEVTDEIMDTDVNCVPCKPGHFQNTSS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KCAFQPPPSCL-----RFV-----QTNISRLLQETSEQLVALKPWITRQNFS 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P--RARCQPHTRC----EIQGLVEAAPGTSYSDTICKNPPEPGAMLLLAILLSLVLFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RCLELQCQPDSSTLPPPWSPRPLEATAP----TAPQPPLLLLLLLPVGLLL---
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 Alphey L., Nurse ation of fission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .08;
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TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               n-LINKED (GLCNAC. . .) (P
29B326A566AEF661 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 87.5;
Pred. No. 3
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                 Glover D.M
cdc2ts and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                      update)
                                                                                                                                                                                                                                                                                                                                                                                                                            479
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.48) (String protein) (Cdc25-like
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 cdc25ts
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                                                                                                         Drosophila embryo.";
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mutants
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FlyBase; FBgn0003525; stg.
InterPro; IPR000751; MPI\_Phosphatase.
InterPro; IPR001763; Rhodanese-like.
Pfam, PF00581; Rhodanese: 1

; A32290; A32290. ; S12008; S12008. ; P30304; 1C25.

M24909; AAA28916.1; -. X57495; CAA40732.1; -. AE003768; AAF56885.1;

PRINTS;

PR00716;

MPIPHPHTASE

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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Brottler P., Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Doson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Ra Colose K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Ra Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Glasser K., Howland T.J., Hernandez J.R., Houck J., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Ra Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Kulp D., Lai Z., Ra Hostin D., Houston K.A., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Ra Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Ra Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.R., Mishina N.V., Mobarry C., Morris J., Moshrefi A., Markulov G., Milshina N.V., Mobarry C., Mornis J., Moshrefi A., Ra McIson D.R., Nelson K.A., Nixon K., Nuxon K., Pacleb J.M., Ra Alazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Ra Alazzolo M., Pittman G.S., Sanders R.D.C., Scheeler F., Shen H., Shen H., Shen E., Spradling A.C., Stapleton M., Strong R. Sur F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T., Spler E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng J. Zheng X.H., Zhong F.N., Zhong W., Zhu S., Zhu X., Smith I Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000)
entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                           use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DOSAGE-DEPENDENT INDUCER MITOTIC CONVENCE. IT IS A TYROSINE PROTEIN PHOSEHATASE REQUIRED PROGRESSION OF THE CELL CYCLE. IT MAY DIRECTLY DEPHOSPHORYLATE P34(CDC2) AND ACTIVATE THE P34(CDC2) KINASE ACTIVITY.
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein tyrosine + phosphate.
-!- SIMILARITY: BELONGS TO THE MPI PHOSPHATASE FAMILY.
-!- SIMILARITY: CONTAINS 1 RHODANESE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  George R.A., Lewis S.E., Richards S., Ashburner M., Henderson Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwani A., An H.-J., Andrews
                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                    the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                identifies two cell cycle genes from Drosophila: a cdc2 homologue and string."; semBO J. 9:3565-3571(1990).
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                                                                                                                     Usage
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Smith H.O.,
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                                                                                                                                                                                                           the developing brain.";

Proc. Natl. Acad. Sci. U.S.A. 91:1819-1823(1994).

-i- FUNCTION: MAY BE INVOLVED IN CELL-CELL INTERACTIONS AND RECOGNITION (BY SIMILARITY).

-i- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.

-i- SUBCELLULAR LOCATION: Type I membrane protein.

-i- TISSUE SPECIFICITY: VARIOUS EMBRYONIC AND ADULT TISSUES; ALSO PROLIFERATIVE ZONES OF THE DEVELOPING BRAIN; HIPPOCAMPAL NEURONS.

-I- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF TYR-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDR1_RAT STANDARD; PRT; 910 AA. 063474; 063474; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Epithelial discoidin domain receptor 1 precursor (EC 2.7.1.112) (Tyrosine-protein kinase CAK) (Cell adhesion kinase) (Tyrosine kinase DDR) (Discoidin receptor tyrosine kinase) (Protein-tyrosine kinase

      SMART;
      SMO0450;
      RHOD;
      1.

      Cell division;
      Mitosis;
      Hydrolase.

      DOMAIN
      319
      A9
      RHODA

      ACT_SITE
      379
      BY SI

      CONFLICT
      228
      228
      A ->

      SEQUENCE
      479
      AA;
      54094
      MW;
      684

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                                                      This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sanchez M.P., Tapley P., Saini S.S., He B., Pulido D., Barbaci "Multiple tyrosine protein kinases in rat hippocampal neurons: isolation of Pk-3, a receptor expressed in proliferative zone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Sprague-Dawley; TISSUE=Brain; MEDLINE=94173920; PubMed=8127887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DDR1 OR EDDR1 OR PTK3
                           between
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                                                                                                                                   KINASES.
SIMILARITY:
SIMILARITY:
  European Bioinformatics
                                                                                                           RECEPTOR SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLVEH
                              SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VTISH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEATAPTA - - - POPPLILLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGLN----
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                                                                                                                                      BELONGS
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Rodentia;
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22.9%;
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Pred.
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                                                                                                                                   '8 TYPE C DON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68483F3A285962CC
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No. 4
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  There are
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Murinae; Rattus
                                                                                                                                      KINASES.
     restrictions
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RESULT 10
DDR1\_MOUSE
ID DDR1\_M
AC Q03146
DT 01-OCT
DT 01-VOU
DT 15-JUN
DE Epithe
DE (Tyros

Q03146; DDR1\_MOUSE

STANDARD;

AΑ

01-OCT-1994 (Rel. 30, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Epithelial discoidin domain receptor 1 precursor (EC

2.7.1.112) (Tyrosine

kinase

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Best Local S
Matches 38
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CARBOHYD
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00231; FA58C; 1.
SMART; SM00219; TYJKC; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; PROSITE; PS00239; RECEPTOR_TYR_KIN_II;
PROSITE; PS01285; FA58C_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                  MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Tyrosine-protein kinase; Glycoprotein; Signal; Phosphorylation; Transmembrane; Receptor; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00059; pkinase; 1.
Pfam; PF00754; F5_F8_type_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001245; Tyr_pkinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                  MOD_RES
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NRPGPREPPPYQEPRPRGTPTHSAPCVPNGSALLL
                                     PRPGEQVPP
                                                                            ILIGCLVAIILLLLIIALML---
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                                                                                                                                                                                                                                    . Similarity
38; Conserv
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                                                                                                                   --PLLLLLLPVGLLLLAAAWCLHWQR----TRRR---
                                                                                                                                                                                                                                                                                                                   910
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24.5%;
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                                                                                                                                                                                                                                       12;
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Pred. No.
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PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
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F5/8 TYPE C
                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC...); 7E7FFA1DCB029806
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                                     -VPSPQDLLL
                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                       35;
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MPK-6)

OR EDDR1 (Discoidin

OR CAK OR MPK6 receptor

tyrosine

kinase) (Protein-tyrosine

kinase

(Mouse)

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THE WAY ARE BURER BY READ DO NOT BE RECORDED TO SERVICE OF A SERVICE O
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Transferase; '...
Phosphorylation; '...
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Pfam; PF00069; pkinase; 1.

Pfam; PF00754; F5_F8_type_C; 1.

Pronom: PD000001; Euk_pkinase;
                                                                                                                                                                                                                                                                                                     SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:99216; Ddrl.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000421; FA58_C.
InterPro; IPR002011; RTKinaseII.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gilardi-Hebenstreit P., Nieto M.A., Frain M., Mattei M.-G., Chestier A., Wilkinson D.G., Charnay P.,
"An Eph-related receptor protein tyrosine kinase gene segmentally expressed in the developing mouse hindbrain.";
Oncogene 7:2499-2506(1992).
-i- FUNCTION: MAY BE INVOLVED IN CELL-CELL INTERACTIONS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L57509; AAB05209.1;
EMBL; X57240; CAA40516.1;
PIR; S30502; S30502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This
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[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6; TISSUE=Embryonic MEDLINE=93096484; PubMed=1281307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coexpressed in breast tumor cell lines oncogene 12:1469-1477(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6;
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[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tyrosine phosphate.

SUBCELLULAR LOCATION: Type I membrane protein.

LALTERNATIVE PRODUCTS: 2 ISOFORMS; CAK I (SHOWN ARE PRODUCED BY ALTERNATIVE SPLICING. THEY ONLY ABSENCE OF A 37 RESIDUES SEGMENT.

TISSUE SPECIFICITY: THE PREDOMINANT ISOFORM CAK DEVELOPING EMBRYO AND ADULT BRAIN; CAK II IS EXECUTED IN CELLS.

SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RECEPTOR SUBFAMILY.
SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: ATP + a protein tyrosine =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RECOGNITION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                            SM00231; FASEC; 1.

SM00231; FASEC; 1.

ES M00239; TYPKC; 1.

FE: PS00107; PROTEIN KINASE_ATP; FALIFIE; PS00109; PROTEIN_KINASE_TYR; 1.

FE: PS0011; PROTEIN_KINASE_DOM; 1.

FE: PS00239; RECEPTOR_TYR_KIN_II; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P00523; 2PTK.
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                                                                                                                              Tyrosine-protein kinase;
                                                                                                     Transmembrane;
                                                                                                                                                          FA58C_1;
FA58C_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=8622863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTERNATIVE
            EPITHELIAL DISCOIDIN DOMAIN RECEPTOR EXTRACELLULAR (POTENTIAL).
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Sciurognathi;
                                                                                                          Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    brain;
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                                                                                                   Glycoprotein; Si
tor; ATP-binding;
                                                                                                                                                                                                                                                                            FALSE_NEG
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thi; Muridae;
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THEY ONLY DIFFE
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S EXPRESSED
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                                                                                                                              Signal;
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RESULT 11
CNG4_BOVIN
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Best Local
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                                                                                                                                                                                                                                        CNG4_BOVIN STANDARD; PRT; 1394 AA.

Q28181; Q28082; Q03861;

Q1-NOV-1997 (Rel. 35, Created)

Q1-NOV-1997 (Rel. 35, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

240 kDa protein of rod photoreceptor CNG-channel (Contains: Glutamic acid-rich protein (GARP); Cyclic-nucleotide-gated cation channel 4

(CNG channel 4) (CNG-4) (Cyclic nucleotide-gated cation channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
VARSPLIC
                                                                                                                SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=96009859; PubMed=7546742;
MCORTSCHEN H.G., Illing M., Seifert R., Sesti
Gotzes S., Colville C., Mueller F., Dose A.,
Kaupp U.B., Molday R.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
cyclic nucleotide-gated cation cha J. Biol. Chem. 271:6349-6355(1996)
                   MEDLINE=96198098; PubMed=8626431;
Biel M., Zong X., Ludwig A., Sautter A.,
"Molecular cloning and expression of the
                                                                                  Kaupp U.B., Molday R.S.;
"A 240 kDa protein represents the nucleotide-gated channel from rod Neuron 15:627-636(1995).
                                         TISSUE=Testis;
MEDLINE=96198098;
                                                                                                                                                                                          Mammalia; Eutheri
Bovidae; Bovinae;
                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                         Bos taurus (Bovine)
                                                                                                                                                                                                                                    CNGB1 OR CNCG4.
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ACT_SITE
                                                               SEQUENCE OF 454-1394 FROM
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474
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Pred. No.
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CYTOPLASMIC
F5/8 TYPE C
POTENTIAL).
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PROTEIN KINASE.
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        channel.";
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                                                                                         photoreceptor.";
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D (GLCNAC...)
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10;
                   modulatory subunit of
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                                                                                                                           F., Willia Godde M.,
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                                                                                                                                     Williams
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                                                                                                                                                                                                              Euteleostomi;
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                                                                                                                          Molday L.,
                                                                                                                                                                                                    Bovoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00888; CNMP_BINDING_1; 1.
PROSITE; PS00889; CNMP_BINDING_2; 1.
PROSITE: PS50042; CNMP_BINDING_3; 1.
Ionic channel; Ion transport; CAMP-b:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00027; cNMP_binding; 1. Pfam; PF00520; ion_trans; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SUBUNIT: FORMS FUNCTIONAL HETEROOLIGOMERIC CHANNELS WITH CNG3
-i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- ALTERNATIVE PRODUCTS: 3 ISOFORMS; CNG4C (SHOWN HERE), CNG4D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sugimoto Y., Yatsunami K., Tsujimoto M., Khorana H.G., Submitted (XXX-1991) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000636; M+channel_nlg
InterPro; IPR000595; cNMP_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Retina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-590 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                   BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Multigene family;
115 PPPSCLRFVQTNISRLL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND CNG4E; ARE PRODUCED BY ALTERNATIVE SPLICING. CNG4D IS BY FAR THE MOST FREQUENT FORM (CNG4D: CNG4C: CNG4E = 20:2:1) IN TESTIS. TISSUE SPECIFICITY: RETINA, TESTIS, KIDNEY, HEART, AND BRAIN. SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X89626; CAA61769.1; -.
X94707; CAA64367.1; -.
M61185; AAA30536.1; -.
                                        35; Conser
                                                                                                                                                                                                                                                                                                                                                                      768
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                                          Conservative
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                                                                                                                                                                1283
1289
1336
                                                       7.0%;
24.6%;
                                                                                                                        155064
                                        13;
                                                                                                                                       R (IN REF. 3).
S -> A (IN REF. 3).
R -> A (IN REF. 3).
D -> E (IN REF. 3).
A -> AA (IN REF. 3).
                                      Score 86.5; DI
Pred. No. 18;
L3; Mismatches
                                                                                                                        WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e splicing.
GLUTAMIC ACID-RICH PROTEIN.
CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL
                                                                                                                                                                                                                                                                 REEEEDEEEEQD -> MR
R -> Q (IN REF. 2
A -> T (IN REF. 3)
                                                                                                                                                                                                                                              VPATEEHPELQVEDADADS ->
                                                                                                                                                                                                                                                                                                                               K -> E (IN REF.
                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (POT MISSING (IN ISOFORM CNG4E). MISSING (IN ISOFORM CNG4D).
                                                                                                                                                                                                                                                                                                                                                                                                            CAMP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                  CAMP (BY SIMILARITY).

CAMP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR H6 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H5 (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cAMP-binding; Transmembrane,
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                                                                                                                        EE6DA559BE3744A7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
  -QETSEQLVALKPWITRQNFSRCL 154
                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                        53;
                                                                                                                                                                                                                                                                                                       MRAGOKGRC (IN REF.
                                                                                                                                                                                                                                                                                      AND 3).
                                                                               Length 1394;
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
                                                                                                                                                                                                                                                GSFQMSPFEALQECEALK
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                                        41;
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ID SSGP_VOLCA
AC P21997;
DT 01-AUG-1991
DT 01-AUG-1991
DT 01-OCT-1996
DE SULFATED 
                                                                         RESULT 13
ATF5_HUMAN
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Best Local S
Matches 21
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DOMAIN 228
DOMAIN 260
SEQUENCE 485 AA;
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01-AUG-1991
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J. Cell Biol. 109:3493-3501(1989).

-i. FUNCTION: THE EXTRACELLULAR MATRIX (ECM) OF VOLVOX CONTAINS INSOLUBLE FIBROUS LAYERS THAT SURROUND INDIVIDUAL CELLS AT A DISTANCE TO FORM CONTIGUOUS CELLULAR COMPARTMENTS. SSG 185 IS MONOMERIC PRECURSOR OF THIS SUBSTRUCTURE (C3Z STRUCTURE), THE COVALENT CROSS-LINKS ARE FORMED BETWEEN THE SACCHARIDE CHAINS RATHER THAN BETWEEN THE POLYPEPTIDE CHAINS.

-i. PTM: A CENTRAL DOMAIN OF 77 AA CONSISTS ALMOST EXCLUSIVELY OF HYDROXYPROLINE RESIDUES.
ATF5_HUMAN
Q9Y2D1; Q9U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-AUG-1991 (Rel. 19, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the EMPL of the support of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A33647; A33647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X51616; CAA35953.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90094551; PubMed=2689458;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             160 PDSSTLPPPWSPRFLEATAPTAPQPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGE 219
                                                                                                                                                                                                                                                     PVPPPPSPPSVL 320
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    Q9UNQ3;
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                                      STANDARD;
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295
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Pred. No. 5.9;
3; Mismatches
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Matches 38
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DOMAIN
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                                                                                                                                             SEQUENCE
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-OCT-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cyclic-AMP-dependent transcription factor ATF-5 (Act
transcription factor 5) (Transcription factor ATFx).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            White J.H., McIllhinney R.A.J., Wise A., Ciruela F., Chan W.Y., Emson P.C., Billinton A., Marshall F.H.; "The GABAB receptor interacts directly with the related transcription factors CREB2 and ATFX.";
                                                                                                                                                            CONFLICT
                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                         SMART; SM00338; BRLZ; 1.
                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:790; ATF5.
                                                                                                                                                                                                                                                                                                                                           EMBL; AF305687; AAG22558.1; -. EMBL; AB021663; BAA78477.2; -. EMBL; AF101388; AAD28370.1; -. TRANSFAC; T04877; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pati D., Meistrich M.L., Plon S.E.; "Human CdC34 and Rad6B ubiquitin conjugating enzymes target repressors of cyclic AMP-induced transcription for proteolysis."; Mol. Cell. Biol. 19:5001-5013(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=20558615;
                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                 Multigene
                                                                                                                                                                                                                                             Pranscription regulation;
                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                     InterPro; IPR004827; TF_bZIP.
Pfam; PF00170; bZIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between
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  179
                                                        144
                               99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CONSENSUS: 5'GTGACGT(A/C)(A/G)-3'), A SEQUENCE PRESENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Nuclear (By similarity). SIMILARITY: BELONGS TO THE BZIP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: BINDS
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                                                       WIT-RONESRCLELQCOPDSSTLPPPWSPRP--LEATA-----
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                                                                                                    Similarity
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ed (DEC-1998) t
                                                                                                                                                                                                                                                             PS00036; BZIP_BASIC;
                                                                                                                                            161
282 AA;
                                                                                                                                                                       123
186
210
236
                                                                                     Conservative
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194
230
250
163
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                                                                                                                                             30674 MW;
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                                                                                                                                                                                                                                             DNA-binding; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ databases
                                                                                                 Score 85;
Pred. No.
                                                                                                                                                        LEUCINE-ZIPPER
                                                                                   Pred. No. 3.9;
7; Mismatches
                                                                                                                                                                                    BASIC MOTIF
                                                                                                                                                                                                     POLY-PRO
                                                                                                                                            DDB2F907CA0215A0 CRC64;
-LLLAAAWCLH--WQRTRRRTPRPGEQ
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3.9;
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                                                                                                                                                           REF
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                                                                                     38;
                                                                                                              Length 282;
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                                                                                     Indels
                                                                                                                                                                                                                                          Nuclear protein;
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RAT
       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                              Structure 6:63-73(1998).

-!- FUNCTION: BINDS TO THE FC REGION OF MONOMERIC IMMUNOGLOBULINS GAMMA. MEDIATES THE SELECTIVE UPFAKE OF IGF FROM MILK AND HELPS NEWBORN ANIMALS TO ACQUIRE PASSIVE IMMUNITY. IGG IN THE MILK IS BOUND AT THE APICAL SURFACE OF THE INTESTINAL EPITHELIUM. THE RESULTANT FCRN-IGG COMPLEXES ARE TRANSCYTOSED ACROSS THE INTESTINAL EPITHELIUM AND IGG IS RELEASED FROM FCRN INTO BLOOD COMPLEXES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE=95059482; PubMed=7969498;
Burmeister W.P., Huber A.H., Bjorkman P.J.;
"Crystal structure of the complex of rat ne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Simister N.E., Mostov K.E., 
"Cloning and expression of the neonatal rat intestinal Fc 
major histocompatibility complex class I antigen homolog." 
Cold Spring Harb. Symp. Quant. Biol. 54:571-580(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                              "Crystal structure Fc.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGG receptor FCRN receptor) (IGG FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1990 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1990
                                                                                                                                                                                                                                                                                                                                          receptor.
                                                                                                                                                                                                                                                                                                                                                      Vaughn D.E., Bjorkman P.
"Structural basis of pH-
                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98154319; PubMed=9493268;
                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 372:379-383(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90315866; PubMed=2534798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Epithelium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "An Fc receptor structurally related to Nature 337:184-187(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simister N.E., Mostov K.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=89097257; PubMed=2911353;
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                                                                                                                         SUBCELLULAR LOCATION: Type I membrane protein. TISSUE SPECIFICITY: INTESTINAL EPITHELIUM. SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
                                                                                                                                                                                     TISSUE FLUIDS (BY SIMILARITY).
SUBUNIT: FCRN COMPLEX CONSIST OF TWO S
IS EQUIVALENT TO BETA-2-MICROGLOBULIN.
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                                                                                                                                                                         HETERODIMER.
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                          (See http://www.isb-sib.ch/announce,
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=BALB/MK X ICR; TISSUE=Brain;
MEDLINE=96194902; PubMed=8654949;
Ido A., Miura Y., Watanabe M., Sakai
                                                                                                                                                                                     ABFI_MOUSE STANDARD; PRT; 3726 AA. 061329; 061329; 06-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) Alpha-fetoprotein enhancer binding protein (AT motif-binding (AT-binding transcription factor 1).
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Mammalia; Eutheria;
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DOMAIN
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SMART; SM00407; IGc1; 1.
PROSITE; PS00290; IG_MHC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 1.
Pfam; PF00129; MHC_I; 1.
                                                                                                 NCBI_TaxID=10090;
[1]
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InterPro; IPR003597; Ig_c1.
InterPro; IPR001039; MHC_I.
                                                                                                                                                                   Mus musculus
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A37374;
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3FRU; 10-JUN-98
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M35495; AAA41611.1;
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51; Conservative
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CYTOPLASMIC (POTENTIAL).

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BY SIMILARITY.

N-LINKED (GLCNAC...) (INLINKED (GLCNAC...
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Pred. No. 5.2;
21; Mismatches
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9A8BF2873A698BB5 CRC64;
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EXTRACELLULAR ALPHA-3.
                                                                                                                               Craniata; Ver
Sciurognathi;
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5.2;
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                                                                                                                                 Muridae;
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PROSITE; PS00028;
PROSITE; PS50157;
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SMART; SM00389; HOX; 4.
SMART; SM00355; ZnF_C2H2; 22.
SMART; SM00451; ZnF_U1; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:99948; Atbf1.
InterPro; IPR001356; Homeobox.
InterPro; IPR00822; znf_C2H2.
InterPro; IPR003604; znf_U1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00046; homeobox; Pfam; PF00096; zf-C2H2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D26046; BAA05046.1; -. HSSP; P20263; 10CP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- FUNCTION: Transcriptional activator sequence of the enhancer element of SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning of the cDNA encoding the Gene 168:227-231(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: CONTAINS 4 HOMEOBOX DOMAINS
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C2H2-TYPE.
HOMEOBOX 4.
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POLY-GLN.
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DOMAIN 3659 3662 POLY-SER.
SEQUENCE 3726 AA; 406567 MW; 915ACBE588A72C98 CRC64;
                                             3225 IPAPQ 3229
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              O9mzv0 canis famil
O9mzu9 felis silve
O9mzu9 felis silve
O9gke0 bos taurus
O8wnv1 bos taurus
O8tl04 mus musculu
O8tch4 mus musculu
O8vch4 mus musculu
O91998 oryza sativ
O99191 leishmania
O99y31 leishmania
O9gy31 leishmania
O9gy31 leishmania
O8vim6 mus musculu
O9n753 leishmania
O9dwh8 rat cytomeg
O9c5t0 arabidopsis
O17889 caenorhabdi
                                                                                                                                                                                                                                                                                                                                    Description
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45	44	43	42	41	40	39	38	37	36	35 5	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
85	85	85	85	85.5	86	86	86	86	86.5	87	87	87.5	87.5	88	88	88	88.5	88.5	88.5	88.5	88.5	89.5	90.5	90.5	90.5	92	92.5	Ñ
6.8		•		٠		6.9			7.0	7.0	7.0	7.0	7.0	7.1	7.1	7.1	7.1	7.1	7.1	•		•		7.3		•	7.4	7.4
1217	413	289	282	795	911	706	299	255	299	5317	510	946	470	753	675	250	1386	1267	404	270	238	474	5120	660	536	251	1400	560
4	11	16	4	σ	11	G	12	11	0	σ	ري د	10	10	12	11	σ	4	10	10	4	16	σı	13	σı	σı	4	G	ر.
Q9P2D0	Q99MM1	Q9A3K1	Q9BSA1	Q95UQ2	035407	Q23600	Q84647	Q9D3J3	Q9TTT9	Q8TA74	044018	022015	Q9LUI1	056971	Q9DBT2	Q9GKE2	075064	Q943D5	Q9AWJ4	Q9UMT1	Q8YWX3	017610	Q9PU36	Q9GY15	Q9GYA0	Q9HAD2	Q8SZS7	Q9GYA1
Q9p2d0 homo sapien	Q99mm1 mus musculu	Q9a3k1 caulobacter		Q95uq2 toxoplasma	O35407 mus musculu	a	Q84647 paramecium	Q9d3j3 mus musculu	Q9ttt9 bos taurus	Q8ta74 hemicentrot	ш				2	Q9gke2 sus scrofa	075064 homo sapien		Q9awj4 oryza sativ	=	Q8ywx3 anabaena sp	017610 caenorhabdi	Q9pu36 gallus gall	Q9gy15 leishmania	Q9gya0 leishmania	N	Q8szs7 drosophila	Q9gyal leishmania

## ALIGNMENTS

9MZV0; 9MZV0; 9MZV0; 9MZV0; 9MZV0; 1-COT-2000 (TrEMBLrel. 15, Created) 1-COT-2000 (TrEMBLrel. 15, Last sequence update) 1-JUN-2002 (TrEMBLrel. 21, Last annotation update) 1-JUN-2002 (TrEMBLrel. 21, Last annotat																															
9MZV0; 9MZV0; 9MZV0; 9MZV0; 9MZV0; 1-COT-2000 (TrEMBLrel. 15, Created) 1-COT-2000 (TrEMBLrel. 15, Last sequence update) 1-JUN-2002 (TrEMBLrel. 21, Last annotation update) 1-JUN-2002 (TrEMBLrel. 21, Last annotat	Qy	Db	Qy	망	Qy	Ma	ğ Ç	SQ	DR	DR	DR	RL	RT	RT	RT	RA	RX	RP	RN	ΟX	8	8	SO	DE	DT	ŊΤ	DT	AC	IJ	OAZM60	RESULT
80 0 0 3;				1 MIVLAPAWSPTASILLLLLLSPGLRGTPDCSFSHSPISSTFAVTIRKLSDYLLQDYPVTV 60	1 MTVLAPAWSPTTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60	182; Conservative 12; Mismatches 35; Indels 7; Gaps	72.1%; Score 895.5; DB 6;	294 AA; 32394 MW;	Pfam; PF02947; flt3_lig; 1.	InterPro; IPR004213; Flt3_lig.	EMBL; AF155148; AAF87088.1;	DNA Seq. 11:163-166(2000).	long cytoplasmic domain.";	degree of similarity to the human and mouse homologue but uniquely	"Molecular cloning of canine and feline flt3 ligand reveals high	Yang S., Sim G.K.;	MEDLINE=20358731; PubMed=10902925;	SEQUENCE FROM N.A.	[1]	•		rdata; Craniata; Vertebrata;	Canis familiaris (Dog).		(TrEMBLrel. 21,	(TrEMBLrel. 15,	-2000 (TrEMBLrel. 15,	Q9MZVO;	9MZV0 PRELIMINARY; PRT;	70	JT 1

Q8vd70 mus musculu

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Best Local 9
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01-MAR-2001
01-DEC-2001
Flt3 ligand
          SEQUENCE FROM N.A.

MEDILINE=20570936; PubMed=11120823;

MWangi W., Brown W.C., Palmer G.H.;

"Identification of fetal liver tyrosine kinase 3 (Flt3) ligand domain

"required for receptor binding and function using naturally occurring
                                                                              Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrai
Mammalia; Eutheria; Cetartiodactyla; Ruminantia;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                        Q9GKEO;
                                                                                                                                                                                                     Q9GKE0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21,
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01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     degree of similarity to the human
long cytoplasmic domain.";
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"Molecular cloning of canine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Flt3 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR004213; Flt3_lig. Pfam; PF02947; flt3_lig; 1. SEQUENCE 291 AA; 32459 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20358731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9685;
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                                                                                                                                                                                                                                                                                                                  RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT
                                                                                                                                                                                                                                                                                                                                                                                                APQAPLILLLLPVALLLMSAAWCLHWRRRRWRTPYPREQ
                                                                                                                                                                                                                                                                                                                                                               ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL
                                                                                                                                                                                                                                                                                                      RFVQTNISHLLQDTSEQLAALKPWITRRNFSGCLELQCQPDSSTPLPPRSPRALEATALP
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                                                                                                                                                                                                                                                                                                                                                    ASNLQDDELCGPFWHLVLAQRWMGRLKAVAGSQMQSLLEAVNTEIHFVTLCAFQPLPSCL
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AF155149; AAF87089.1; -.
   isoforms
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01 (TremBLrel. 19, La
d isoform-1.
(Bovine)
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80.5%;
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Pred. No. 4.3e-80;
9; Mismatches 33;
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                                                                                                     Vertebrata; Eute.
minantia; Pecora;
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                                                                                                                   Euteleostomi;
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Best Local
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Q1-MAR-2002 (TrEMBLrel. 20, C
Q1-MAR-2002 (TrEMBLrel. 20, I
Q1-JUN-2002 (TrEMBLrel. 21, I
Flt3 ligand.
FLT3 LIGAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Immunol. 165:6966-6974(2000).

EMBL; AF282985; AAF99322.1; -.

InterPro; IPRO04213; Flt3_11g.

Pfam; PF02947; flt3_11g; 1.

SEQUENCE 292 AA; 32390 MW; D
                                                                                                                                                                                                                                                            Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases EMBL; AB051841; BAB79634.1; -. InterPro; IPR004213; Flta_liq. Pfam; PF02947; Flt3_liq; 1. SEQUENCE 292 AA; 32388 MW; 2A797E0C1199C1D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthoria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8WNW1
                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                             Hikono H., Momotani E.;
"Cloning of a cDNA for bovine
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
181
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PGPQSPLLLLLLLLLPVALLLLATAWCLCRWRRRRTRYPGER
                       TAPOPP----LLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQ 220
                                                              LREVQTNISRLLQETSEQLVALKPWITRQNESRCLELQCQPDSSTLPPPWSPRPLEATAP
                                                                                                      VASNLQDDKLCGAFWRLVLAQRWMGRLKTVAGSEMEKLLEDVNTEIHFVTSCAFQPLPSC
                                                                                                                  VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVIKCAFQPPPSC
                                                                                                                                                     MTVLAPAWSPTT-YLLLLLLLSSGLSGTODCSFQHSPISSDFAVKIRELSDYLLQDYPVT
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                                               \tt LRFVQANISHLLQDTHQQLEALKPWITHRNESRCLELQCQPDSPTLLPPRSPGALGATSL
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75.9%;
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76.38;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                         Score 835; DB 6;
Pred. No. 3.2e-74;
2; Mismatches 38
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                                                                                                                                                                                                                                                                                                                             flt3 ligand."
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Best Local
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01-DEC-2001
Flt3 ligand
                                                                                                                                                                                                                                           01-NOV-1996
01-NOV-1996
01-JUN-2002
                                                                     SEQUENCE FROM N.A.

MCClanahan T., Culpepper J., Campbell D., Wagner J., Fr.

Mattson J., Tsai S., Luh J., Guimares M.J., Mattei M.-G

Birnbaum D., Hannum C.;

"Flt3 ligand: expression, genomic organization, alterna

forms and processing.";

Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases
           EMBL; U44024; AAA93305.1; ...
MGD; MGI:95560; F1t31.
InterPro; IPR004213; F1t3_lig.
InterPro; IPR001230; Prenyl_site.
Pfam; PF02947; f1t3_lig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mwangi W., Brown W.C., Palmer G.H.;
"Identification of fetal liver tyrosine kinase 3
required for receptor binding and function using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9GKD9;
01-MAR-2001
                                                                                                                                                                                Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                             Q61104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF282986; AAF99323.1; -. InterPro; IPR004213; Flt3_lig. Pfam; PF02947; flt3_lig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20570936; PubMed=11120823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9GKD9
                                                                                                                                                                     NCBI_TaxID=10090
                                                                                                                                                                                                       Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                         163
                                                                                                                                                                                                                                                                                                                                                                              180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gand isoforms.";
Immunol. 165:6966-6974(2000).
                                                                                                                                                                                                                               ligand,
                                                                                                                                                                                                                                                                                                                                                      PGPQSPLLLLLLLLLPVALLLLATAWCLCRWRRRRTRYPGER
                                                                                                                                                                                                                                                                                                                                                                                                                 LRFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MTVLAPAWSPTT-YLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVT
                                                                                                                                                                                                                                                                                                                                                                             TAPOPP----LLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                     VASNLQDDKLCGAFWRLVLAQRWMGRLKTVAGSEMEKLLEDVNTEIHFVTSCAF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MTVLAPAWSPTTSLLLLLLLSPGLQGTPDCSFRHSPISSTFAIKIGKLSKYLLQDYPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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1 (TrEMBLrel.
1 isoform-2.
                                                                                                                                                                                                                                 (TrEMBLrel.
(TrEMBLrel.
1, T169 form.
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                                                                                                                                                                                                                                                                    (TrEMBLrel.
                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                      -QDTHQQLEALKPWITHRNFSRCLELQCQPDSPTLLPPRSPGALGATSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos.
PRENYLATION; UNKNOWN_1
                                                                                                                                                                                  Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30372 MW;
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19,
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21,
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Last annotation update)
                                                                                                                                                                                                                                                                    Created)
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                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  725A7F77A95DA98B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                     Wagner J., Fra
., Mattei M.-G.
                                                                                                                                                                                                                                             update)
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                                                                                              alternatively
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         274;
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                                                                                                                      Rosnet
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RESULT
Q8VCH4
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Q9LGG8
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Best Local S
Matches 120
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                                                    Q1IGG8;
01-OCT-2000 (TrEMBLrel. 15, Create
01-OCT-2000 (TrEMBLrel. 21, Last
01-JUN-2002 (TrEMBLrel. 21, Last
Putative extensin-like protein.
P0406H10.6 OR OJ1174_D05.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8VCH4 PRELIMINARY; PRT; 169 AA.
Q8VCH4;
Q8VCH4;
Q1-mAR-2002 (TrEMBLrel. 20, Created)
Q1-mAR-2002 (TrEMBLrel. 21, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to FMS-like tyrosine kinase 3 ligand.
                                                                                                                                                                                                                                                                                                                                                                                               Kinase.
SEQUENCE
Oryza sativa (Rice). Eukaryota; Viridiplantae; Streptophyta; Enspermatophyta; Magnoliophyta; Liliopsida; Ehrhartoideae; Oryzeae; Oryza. NCBI_TaxID-4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted DEC-2001) to the EMBL/GenBank/DDBJ EMBL; BC019801; AAH19801.1; -. InterPro; IPR004213; Flt3_lig. Pfam; PF02947; flt3_lig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                     Q9LGG8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                                                                                                                           MTVLAPAWSP-TTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVT
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                                                                                                                                                                                                             LRFVQTNISRLLQETSEQLVALKPWITR--QNFSRCLELQCQPDSSTLPPPWSPR
                                                                                                                                                                                                                                                                                                 MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
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72.6%;
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Last sequ
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Pred. No. 1.5
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Pred. No. 3.7e-49;
4; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
                                                                                                                                      PRT;
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                          Embryophyta; Tracheophyta; Poales; Poaceae;
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RESULT
Q9GY11
ID Q9
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DT Q9
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DT Q9
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Best Local
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Pfam; P000560; LRR; 6.
PRINTS; PR01582; KV33CHANNEL.
PRINTS; PR01217; PRICHEXTENSN.
SMART; SM00370; LRR; 5.
PROSITE; P500030; RRM_RNP_1; UNKNOW
SEQUENCE 579 AA; 62607 MW; 0445
                                                                                                                                                                                        STRAIN=FRIEDLIN;
Murphy L., Quail M., Harris D.,
Oliver K.;
                                                                 InterPro; IPR000561; EGF-like.
InterPro; IPR001611; LRR.
InterPro; IPR002965; P_rich_ex
                                                                                                                                       Submitted (AUG-2001) to the EMBL/GenBank/DDBJ EMBL; AL390114; CAC02038.2; -.
                                                                                                                                                                                                                                                                                                                             Leishmania major.
Eukaryota; Euglenozoa;
                          PRINTS;
                                                Pfam; PF00560; LRR; 6.
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                LM12.156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9GY11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Oryza sativa nipponbare(GA3) genomic DNA, chromosome clone:p0406H10.";
                                                                                                                                                                                                                                                                                                       NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases EMBL; AP002524; BAB07956.1; -. EMBL; AP003118; BAB33013.1; -. InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sati wa nipponbare(GA3) genomic DNA,
clome.orill7, nos "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CV. NIPPONBARE; Sasaki T., Matsumoto T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003592; LRR_out.
InterPro; IPR002965; P_rich_extensn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JAN-2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       392 PSPPPP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 TAPQPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSP 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                283 VAGMRKVEQL-DVAHNLLTGAIPQAVCELPRLKNFTFAYNFFTGEPPSCAHAVPRYGDRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 ILLINTGLS-----SCLPPEVGM-LREVTVF-----DVSFNRLAGPLPSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 LLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCLPNRPAQRTLRQCAAF-----FARPPVNCAAFQCKPFVPALPPPSPPPP--SPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQ-----PPPSCLRFV----QT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NI--SRLLQETSEQLVALKPWITRQNFSR----CLELQCQPDSSTLPPPWSPRPLEATAP
  SM00181; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
  ; PRICHEXTENSN EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRM_RNP_1; UNKNOWN_1.
; 62607 MW; 04457E18E7405AAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.1%;
23.7%;
                                                                 P_rich_extensn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ť
                                                                                                                                                                                                                                                                                                                             Kinetoplastida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28;
                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 112.5; DB 10; Pred. No. 0.013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                         Rajandream M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  668 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -SPPPPSTSPPPPSP
                                                                                                                                                                                                                                                                                                                          Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69;
                                                                                                                                                             databases
                                                                                                                                                                                                         Ivens A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    411
                                                                                                                                                                                                           Barrell
                                                                                                                                                                                                                                                                                                                             Leishmania.
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RESULT 10
Q9GY33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
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                                                                                                                                                                                                                Query Match
Best Local S
Matches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                               Submitted (AUG-2001) to the EMBL/GenBank/DDBJ EMBL; AL390114; CAC02017.2; Interpro; IRR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                          Murphy L., Quail M., Oliver K.;
                                                                                                                                                                                                                                                                                                            InterPro; IPR002965; P_rich_extensn.
Pfam; PF00560; LRR; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16,
01-OCT-2001 (TrEMBLrel. 18,
01-JUN-2002 (TrEMBLrel. 21,
probable surface antigen p2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9GY33 PRELIMINARY;
Q9GY33;
01-MAR-2001 (TrEMBLrel.
01-OCT-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                 PRINTS; PR01217; PRICHEXTENSN SMART; SM00181; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-FRIEDLIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Euglenozoa; Kinetoplastida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leishmania major
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  289
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VSGTLPPEWSSMGSLANLQLSLTQVSGTLPPQWSSMKKLTQLLLTDTLLSGTLPAEW 345
                                                                                                                                                            LPPEWSSMPNLNAVELKRLKLSGT------LPADWS-SLKSLSNVVLEDMPIT----
                                                                                                                                                                                    LAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASN 63
                         DSSTLPPPWSPR-----PLEATAPTAPQPP-----LLLLLLLPVGLL--LLAAAW 203
                                                  ALRFLTLDGTNLSGTLPPQWSAMASVISLNLEGTEVSGTLPPEWISMSRL-QTLNLRRTK 288
                                                                              CLRFVQ---TNISRLLQ-----
                                                                                                                                 LQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPP-----S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VSGTLPPEWSSMGSLANLQLSLTQVSGTLPPQWSSMRKLTQLLLTDTLLSGTLPAEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSSTLPPPWSPR-----PLEATAPTAPQPP-----LLLLLLPVGLL--LLAAAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALRFLTLDGTNLSGTLPPQWSAMASVISLNLEGTEVSGTLPPKWISMSRL-QTLNLRRTK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPPEWSSMPNLQTLQVRRLKLSGT-----LPADWS-SLKSLSNVVLEDMPIT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLREVQ---TNISRLLQ------ETSEQLVALKP-WITRQNESRCLELQCQP 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPP----S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63;
                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                     648 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    668 AA;
                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                        LPPEW--
                                                                                                                                                                                                                                                                     68470 MW; 8EB78AC101E01286 CRC64;
                                                                                                                                                                                                                           8.3%;
26.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70725 MW; CEB3ECAABC490C94 CRC64;
                                                                                                                                                                                                                                                                                                                                      LRR.
                                                                                                                                                                                                                                                                                                                                                                                                     Harris D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.4%; Score 104.5;
26.6%; Pred. No. 0.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation updat
                                                                                                                                                                                                              Score 102.5; D
Pred. No. 0.14;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                     Rajandream M.,
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Mismatches
                                                                            ETSEQLVALKP-WITRONFSRCLELQCQP 160
                                                                                                        GSLERIQQLVLRKLKVTGPLPPQWSPMK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -GSLERIQQLVLRKLKLTGPLPPQWSPMK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trypanosomatidae; Leishmania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA
                                                                                                                                                                                                                                         DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 5;
                                                                                                                                                                                                             77;
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                                                                                                                                                                                                                                                                                                                                                                            databases
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                                                                                                                                                                                                                                                                                                                                                                                                     Barrell
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                                                                                                                                                            194
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RESULT Q8VIM6

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RESULT 12
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Best Local :
Submitted (AUG-2001) to the EMEL; AL390114; CAB98658.2; -. InterPro; IPR001611; LRR. InterPro; IPR003592; LRR_out. Pfam; PF00560; LRR; 3. SMART; SM00370; LRR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002
01-MAR-2002
01-JUN-2002
                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 01-OCT-2001 (TrEMBLrel. 01-DEC-2001 (TrEMBLrel.
                                                              Murphy L., Quail M., Oliver K.;
                                                                                                               Leishmania major.
Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
                                                                                                                                                                                               Q9N753;
                                                                                                                                                                                                           Q9N753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Verpy E., Masmoudi S., Zwaenepoel I., Leibo
Del Castillo I., Nouaille S., Blanchard S.,
Moreno F., Mueller R.F., Petit C.;
"Mutations in a new gene encoding a protein
non-syndromic deafness at the DFNB16 locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8VIM6;
                                                                                 STRAIN-FRIEDLIN;
                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                        Probable surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stereocilin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21547528; PubMed=11687802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGI:2153816;
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AF375593; AAL35321.1; -
                                                                                                                                                                                                                                                            TTPRPPPTTPQPPPTTTQPIP--
                                                                                                                                                                                                                                                                         AT---APTAPQPPLLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVP-PVPS
                                                                                                                                                                                                                                                                                                    PRASQPAAHISP --
                                                                                                                                                                                                                                                                                                                                                                                                                                                VLAPAWSPTTYLLL------LLLL------SSGLSGTQDCSFQHSPISSDFAVKIRE 47
                                                                                                                                                                                                                                                                                                                       QETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPP-----
                                                                                                                                                                                                                                                                                                                                          GQPEPDASGQCQGGNLQQLLLWGMRNNLSWDARALGFLSGSPPPPPPALLHCLSRGVP--L
                                                                                                                                                                                                                                                                                                                                                                                   PAPHFLQGLLGLLTPAGELGSEEALWGGLLRTVGAPLYAAFQEGLLRVTHSLQDEVFSIM
                                                                                                                                                                                                                                                                                                                                                                                                       LSDYLLQDY -- PVTVASNLQDEE-LCGGLWRLV---LAQRWMERLKTV------
                                                                                                                                                                                                                                                                                                                                                                                                                            VLAADWLPSLMLLLEGTRWQALVQLQPSVDPTNATGLDG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1809 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.A.
                                                                                                                                                       antigen
                                                                                                                                                                                                                                                                                                                                                             AGSKMQGLLERVNTEIHFVTKC-----AFQPPPSCLRFVQTNISRLL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                  RQRRAISVEALCENHSGPEPPYSISNFSIYLLCQHIKPATPRPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.1%;
23.7%;
                                                                        Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              196404 MW;
                                                                                                                          Kinetoplastida;
                                                                                                                                                               15,
18,
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20,
21,
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Last anno
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                                                  EMBL/GenBank/DDBJ
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 100.
Pred. No.
                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blanchard S., Laine
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Sciurognathi;
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; Murinae; Mus
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                                                                                                                        Leishmania
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Q9C5T0;
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01-JUN-2001
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01-MAR-2001
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Virus Res. 69:119-130(2000).
EMBL; AF232689; AAF99111.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat cytomegalovirus (strain Maastricht)
Viruses; dsDNA viruses, no RNA stage; H
Betaherpesvirinae; Muromegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=MAASTRICHT;
MEDLINE=20473137; PubMed=11018281;
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33.0%;
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EMBL: AF224705; AAK28315.1; -.

InterPro: IPR002902; DUF26.

InterPro: IPR002719; Euk_pkinase.
InterPro: IPR002719; Ser_thr_pkinase.
InterPro: IPR001290; Ser_thr_pkinase.
InterPro: IPR00125; Jer_pkinase.
Pfam; PF001657; DUF26; 2.
Pfam; PF001657; DUF26; 2.
                                                                                                                                                                                                                                                                               O17889;
01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
"Genome sequence of the nematode C.elegans: investigating biology."; Science 282.2012-2018(1998).
EMBL; Z81546, CAB04464.1; -.
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PROSITE; PS50011; PROTEIN_KINASE_DOW; 1.
ATP-binding; Kinase; Transferase.
SEQUENCE 658 AA; 72991 MW; DCF9CF5F1748F614 CRC64;
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SMART; SM00220; S_TKC; 1.
SMART; SM00219; TyrKC; 1.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                        SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                         SEQUENCE FROM N.A. Barlow K.;
                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                  Caenorhabditis elegans.
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                                                               none;
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                                                                                                                                                                                      NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 LVALKPWITRQNFSRCLEL---QCQPD------STLPPPWSPR 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      -GEQVPPVPSPQ 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPSISTPPVSAPPRSEKEGNSKVLVIAIVVPIIVAVRLFIAGYCFLTRRARKSYSTPSAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVQCTPDLTRQDCSRCLQLVINQIPTDRIGARIINPSCTSRYEIYAFYTESAVPPP--PP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen Z.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.5%;
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                                                                                                                                                                                                                                                                                 05,
20,
                                                                                                                           the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Mismatches
                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 93.5;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                               1217 AA
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                                           A platform
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                                              for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217
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Query Match
Best Local Similarity
***ches 38; Conserva
Search completed: November 24,
Job time : 31.2232 secs
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                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; TYT_P:
Pfam; PF00102; Y_phosphatase; 1.
SMART; SM00194; PTFC; 1.
SMART; SM00194; PTFC; 1.
PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS00155; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; :
                                                                                                                                                                                                                                                                                                                                               Hydrolase.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P18052; 1YFO
                                                                     743
                                                                                                                                                                       140
                                                                                                     192 LPVGLLLLAA-----AWCLHWQRTRRRTPRPGEQVPPVPSP
                                                                                                                                       683 ALRPQPTTSDPTAAAPVPIPNNKGSLNGNPSPSSPPLLPPVASSTPAATPEESNMLLYII 742
                                                                                                                                                                                                           627 MDAVKAVDGTKYSSVIDALEKLSTMDLDFQKYKFKEAPATLKAMDL----FFASYASNLA 682
                                                                                                                                                                                                                                          83 MERLKTVAGSKMQCL---LERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLV 139
                                                                     GAVGGLLVVAIIGVILFFVFFQKKKKKEDKPDD--PPAPLP
                                                                                                                                                                      ALKPWITRONFSRCLELOCOPDSSTL---PPPWSPRPLEATAPTAP-----QPPLLLLLL 191
                                                                                                                                                                                                                                                                                                                                               1217 AA; 135500 MW;
                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                             7.5%; Score 93; DB 5; 23.6%; Pred. No. 2.6;
                 2002,
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                                                                                                                                                                                                                                                                               Mismatches
                   10:11:38
                                                                                                                                                                                                                                                                                                                                               1D1656F460E38508 CRC64;
                                                                                                                                                                                                                                                                               68;
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                                                                                                       227
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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         10
10
                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                               Score
         1242
1242
1242
1242
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1236
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length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                  Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A_Geneseq_101002:*
1: /SIDS2/gcgdata/;
2: /SIDS2/gcgdata//
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        November 24, 2002, 10:02:26; Search time 31.7704 Seconds (without alignments) 985.632 Million cell updates/sec
         100.0
100.0
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1242
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                                                                                                                                                                                                                                                                                                                                                                          7: //SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT: *
8: //SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT: *
9: //SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT: *
9: //SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT: *
10: //SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT: *
11: //SIDS2/gcgdata/geneseq/geneseqp-emb1/AA199.DAT: *
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13: //SIDS2/gcgdata/geneseq/geneseqp-emb1/AA199.DAT: *
14: //SIDS2/gcgdata/geneseq/geneseqp-emb1/AA199.DAT: *
15: //SIDS2/gcgdata/geneseq/geneseqp-emb1/AA199.DAT: *
16: //SIDS2/gcgdata/geneseq/geneseqp-emb1/AA199.DAT: *
17: //SIDS2/gcgdata/geneseq/geneseqp-emb1/AA199.DAT: *
18: //SIDS2/gcgdata/geneseq/geneseqp-emb1/AA199.DAT: *
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21: //SIDS2/gcgdata/geneseq/geneseqp-emb1/AA199.DAT: *
22: //SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT: *
23: //SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT: *
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Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
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       AAR67541

AAW67769

AAY620192

AABB08129

AABB08129

AAB66175

AAR661791

AAW69007
                                                                                                                                                                                                                                                                     SUMMARIES
Human flt-3 ligand
Human flt3-ligand.
Full length wild t
Human Flt-3 ligand
Human Flt3L polype
Human S86/S109 Flt
Human flt-3 ligand
Human flt-3 mutein
Human flt-3 recept
Mature wild type h
                                                                                                                                                                                                             Description
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45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
w	w	ω	w	w	36.	36.	36.	737.5	37.	w	739		4	4	σ,	768	8			Ξ.		7.	ü	894.5		970	1100	1107	1108	1108	1110	1110	1110	1110
														•								•	•	72.0	•	•	•	•	•	•	•	89.4	89.4	89.4
313	144	144	140	140	523	349	340	349	349	143	143	377	150	150	232	232	231	231	231	265	276	268	178	291	294	185	209	209	209	209	209	209	209	209
19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	22	16	22	20	16	21	21	21	22	21	21	22	21	21	21	21	21	21	21	21
AAW83294	AAW69052	AAW77928	AAW69035	AAW77911	AAW78008	AAW83286	AAW83291	AAW78005	AAW83289	AAW69050	AAW77926	AAW78124	AAW69054	AAW77930	AAB20189	AAR66177	AAB20186	AAW67768	AAR67540	AAY58211	AAY58207	AAY58206	AAB20193	AAY58210	AAY58204	AAB20195	AAY69725	AAY69728	AAY69724	972	AAY69729	72	697	AAY69723
_	Human flt-3 recept			1t3	C E	G		F1t3L 1-139/IgG2b/	flt3	flt	Flt3 ligand FLT3C.	Chimeric receptor	Human flt-3 recept		Mouse Flt-3 ligand	MOT11(	Mouse Flt-3 ligand	Murine flt3-ligand	Mouse flt-3 ligand	Feline mature Flt-	Canine Flt-3 ligan	matur	Human Flt-3 ligand	w	ω	Human Flt-3 ligand	Human flt-3 mutein	Human flt-3 mutein	$\mathbf{L}$	1t-3	flt-3	Human flt-3 mutein	flt-3 mute	Human flt-3 mutein

## ALIGNMENTS

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RESULT 1
AAR67541
ID AAR6
07-DEC-1994.
                                                                              Domain
                                                                                                              Domain
                                                                                                                                                            Homo sapiens.
                                                                                                                                                                             Flt-3 ligand; flt3-L; anemia; cancer; AIDS; gene therapy
                                                                                                                                                                                            Human flt-3 ligand
                                                                                                                                                                                                             05-AUG-1995 (first entry)
                                                                                                                                                                                                                              AAR67541;
                                                                                                                                                                                                                                             AAR67541 standard; Protein; 235
      19-MAY-1994;
                                      EP627487-A.
                                                              Domain
                                                                                                                                     Peptide
      94EP-0303575
                                                                                                           /label= Sig_peptide
/note= "signal peptide may extend
27...182
                                                              206.
                                                                               183..205
                                                                                    /label= Extracellular_domain
/note= "extracellular domain may
position 28"
                                                     /label= Cytoplasmic_domain
                                                              /label= Transmembrane_domain
206..235
                                                                                                                                             ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Qγ
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12-AUG-1993;
25-AUG-1993;
03-DEC-1993;
07-MAR-1994;
11-MAY-1994;
                                                                                                                                      Antigen-specific peripheral immune tolerance; flt3-ligand; flt3-L; immunogenic; autoimmune disease; organ transplantation; food aller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A human T-cell lambda-gt10 random primed cDNA library was screened with a fragment corresponding to the extracellular domain of mouse flt3 ligand (flt3-L) (nt 103-516 of AAQ79076) to isolate human flt3-L cDNA. Flt3 stimulates progenitor and
                       17-JUN-1997;
                                           12-JUN-1998;
                                                                                                                                                                       Human flt3-ligand
                                                                                                                                                                                             25-MAR-1999
                                                                                                                                                                                                                                     AAW67769 standard;
(IMMV ) IMMUNEX CORP.
                                                                                                                              tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated ligands for flt 3 receptors - anaemia, AIDS and various cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ( VMMI)
                                                                                                                                                                                                                                                                                       181 APQPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH
                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
235;
                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                         sapiens
                                                                                                                                                                                                                                                                                                     APQPPLLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH
                                                                                                                                                                                                                                                                                                                                  REVQTNISRLLQETSEQLVALKPWITRQNESRCLELQCQPDSSTLPPPWSPRPLEATAPT
                                                                                                                                                                                                                                                                                                                                             RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT
                                                                                                                                                                                                                                                                                                                                                                                       ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                               MTVLAPAWSPTTYLLLLLLLSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1995-008071/02
                                                                                                                                                                                                                                                                                                                                                                           ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cells,
                                                                                                                                                                                                                                                                                                                                                                                                                    MTVLAPAWSPTTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV
                                                                                                                             transplantation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ79079.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        235 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 29-30;
                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93US-0068394.
93US-0106463.
93US-0111758.
93US-0162407.
94US-0209502.
94US-0243545.
                       97US-0877421
                                           98WO-US12085
                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         be used e.g. in gene therapy protocols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33pp; English
                                                                                                                                                                                                                                     235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1242; DB :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                       allergy;
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RESULT 3
AAY69719
ID AAY6
XX AAY6
AC AAY6
XX AY7
AC DT 05-J
XX Full
XX Immu
KW Immu
KW Immu
KW cell
KW cell
KW cell
KW cell
KW cell
KW myel
KW myel
KW myel
KW myel
SY Homo
XX Homo
XX
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                                                                                                                                                                                                                                     Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV; neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy; cell surface tyrosine kinase receptor; hematopoietic progenitor cell; cellular expansion; cellular differentiation; natural killer cell; cancer; dendritic cell; immune response; autoimmunity; immunosuppression; myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or therapeutic molecule, respectively. The polypeptide is capable of binding the flt3 receptor and is: a) amino acids 28-x of murine flt3 ligand (flt3-L), where x is an amino acid between 163-231; b) amino acids 28-y of human flt3-L, where y is an amino acid between 160-235; and c) a polypeptide that has at least 90% identity to the polypeptides of either (a) or (b). The method ameliorates the effects of autoimmune diseases, food allergies or organ or tissue rejection following transplantation. Administration of flt3-L allows lower doses of antigens to be used in vivo for mucosally administered antigens. The present
                                                                                                                                                                                                            myelodysplasia; aplastic anemia;
multiple myeloma; leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A method has been developed of initiating or enhancing: (i) an antigen-
specific immune tolerance; or (ii) immunotolerance of a therapeutic
immunogenic molecule by addition of a polypeptide, before, after or with
the mucosal administration of an immunotolerising amount of the antigen
                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Full length wild type human flt-3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY69719 standard; Protein; 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence represents human flt3-L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Abbott NM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APQPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 14-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        235 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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Pred. No. 5e-109;
; Mismatches 0
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expansion (especially in vivo) or differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic cells, especially in the presence of growth factors such as interleukins, colony stimulating factors or protein kinases. The protein can also modulate, augment or enhance a patient's immune response and can be used to treat an immune rentain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  which exhibits increased or decreased biological activity relative to the full length wild type (this sequence) or mature (AAY69720) flt3-L polypeptides. The flt3-L protein binds cell surface tyrosine kinase receptors and regulate growth and differentiation of hematopoietic progenitor cells. The flt3-L protein can be used to induce cellular
                                             Flt-3 ligand; Fms-like tyrosine kinase; human; vacimmunotherapy; therapy; tumour; cancer; melanoma; lymphoma; autoimmune disease; infection; gene the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorder (e.g. allergy, autoimmunity or immunosuppression). The protei may be used to treat a pathological condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast, small cell lung, testicular or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mutant soluble flt3 ligand polypeptide used in cellular expansion, immune response stimulation or treatment of pathological condition contains amino acid substitutions at positions 8, 84, 118 or 122
                                                                                                              Human Flt-3 ligand
                                                                                                                                                                                AAB20192;
                                                                                                                                                                                                               AAB20192 standard; Protein; 235 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 72-73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IMMV ) IMMUNEX CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention relates to novel soluble flt3 ligand (flt3-L) polypeptides the exhibits increased or decreased biological activity relative to
                                                                                                                                                                                                                                                                                                             APQPPLLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLLVEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MTVLAPAWSPTTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV
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                                                                                                                                                                                                                                                                                               APQPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH
                                                                                                                                                                                                                                                                                                                                                                                              RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT
                                                                                                                                                                                                                                                                                                                                                                                                                              ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL
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                                                                                                                                            entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1242; DB 21,
Pred. No. 5e-109;
                                                                             human; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                         suppressing tumour growth in a mammal. The tumour is melanoma, glioma or lymphoma, particularly B-cell mynhoma. They can also be used for the prophylactic and/or therapeutic treatment of:

(a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B and C in humans), parasitic (e.g. malaria) and fungal infections;
                                                                                                                                                                                                                                                         polynucleotide may encode the present full-length human Fit-3 ligand polypeptide, or amino acids 27-160, 1-160, 27-185, 1-185, or 27-235 of the ligand. The polynucleotides are incorporated into the cells of the vertebrate in vivo, and a prophylactically or therapeutically effective amount of Fit-3 ligand and 1 or more antigens or cytokines is produced in vivo. Pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                     (Fit-3 ligand). The invention is directed to enhancing the immune response of a vertebrate to an antigen or a cytokine by administering in vivo, into a tissue of a vertebrate, a Fit-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunogenic compositions comprising Flt-3 ligand encoding polynucleotide and one or more antigen, or cytokine encoding polynucleotides, useful for suppressing tumour growth and for treating
                                                               Sequence
                                                                                               specification
                                                                                                             Various other examples of these diseases are given in the
                                                                                                                          (b) autoimmune diseases (e.g. rheumatoid arthritis and
osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
                                                                                                                                                                                                                                             compositions comprising the polynucleotides are useful
                                                                                                                                                                                                                                                                                                                                                          cytokine-encoding polynucleotides.
                                                                                                                                                                                                                                                                                                                                                          ligand-encoding polynucleotide, and 1 or more antigen- or cytokine-encoding polynucleotides. The Flt-3 ligand-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is that of human Fms-like tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 132-133; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      autoimmune diseases (e.g. rheumatoid arthritis)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAF30310
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   235;
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   Conservative
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27..235
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27..182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Extracellular_domain
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Score 1242; DB 22
Pred. No. 5e-109;
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                                                                                                                                                                                                                                                                     CC involves administering a combination of two to five agents. The method CC agent; (c) dendritic cell mobilisation factor; (b) dendritic cell mobilisation factor; (b) dendritic cell maturation CC agent; (c) dendritic cell activation agent; (d) T cell enhancing factor; CC or (e) activated, antigen-specific T cells. The methods are useful for CC treating an individual at risk for or suffering from infection with a CC pathogenic or opportunistic organism, e.g. viruses (e.g. HIV), bacteria CC (e.g. M. tuberculosis), yeast, fungi (e.g. C. albicans) or protozoa (e.g. CC T. cruzi, which causes Chaga's disease). The methods are especially CC useful for treating an individual suffering from immunosuppression by CC enhancing a lymphocyte-mediated immune response. In particular, the CC method is useful for treating inflammations, chickenpox, oral or genital CC trepes, mononucleosis, multifocal leukoencephalopathy, hepatitis, AIDS, CT cell leukemia or T cell lymphoma. The activated antigen-presenting CC dendritic cells are useful as a vaccine adjuvant. The present sequence CC represents a human Flt3L polypeptide fragment, that can be used as a CC dendritic cell mobilisation factor.
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                                                                                                                    Matches
                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rreating an individual suffering from infection, e.g. inflammation, chickenpox or AIDS, by administering a combination of dendritic cell mobilization factor or maturation agent, T cell enhancing factor and antigen-specific T cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lynch DH,
Thomas EK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 37-38; 43pp;
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                                                                                                                                                Local Similarity
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                           MTVLAPAWSPTTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
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MTVLAPAWSPTTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV
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llarity 100.0%;
Conservative
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                                                                                                                 Score 1242;
Pred. No. 5e-
0; Mismatches
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                                                                                                     e 1242; DB 25,
No. 5e-109;
0;
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RESULT 6
AAR66175
ID AAR6
C MRIBS, was screened with an 800 bp fragment derived from pMRIBS, was screened with an 800 bp fragment derived from conserved between two mouse clones, TilB and TilO. Approx. 20 conserved between two mouse clones, TilB and TilO. Approx. 20 conserved between two mouse clones, TilB and TilO. Approx. 20 cones, S86 and S109, were found to be approx. 75% homologous to the mouse clones over the first 163 AAs. Clone S86 continued to be approx. 75% homologous to the mouse clones over the first 163 AAs. Clones S10 continued to be approx. 75% homologous to show homology to TilO until the stop codon, although to a lesser degree, for an overall homology of 66%. Clones TilB and S109 do not show homology to each other or to the other clones after mouse residue 163 (human residue 160). An additiona mouse clone designated MBB has a 29 AA insert at the junction between the common and divergent portions of the mouse ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-MAY-1993;
07-JUL-1993;
16-JUL-1993;
13-AUG-1993;
24-AUG-1993;
19-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                      New ligand for the FIt3 tyrosine kinase receptor - and related nucleic acid, vectors, host cells and antibodies, useful for treating abnormal cell physiology and proliferation, e.g. cancer, also for diagnosis and drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                         A cDNA library from the human stromal cell line 29SV48, in
                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 76-77; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Birnbaum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human S86/S109 Flt3 ligand peptide sequence
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93US-0089263.

93US-0092549.

93US-0106340.

93US-0112391.

93US-0155111.

93US-0162413.
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Sequence

235

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                                                     Immunogenic compositions comprising Fit-3 ligand encoding polynucleotide and one or more antigen, or cytokine encoding polynucleotides, useful for suppressing tumour growth and for autoimmune diseases (e.g. rheumatoid arthritis).
The present sequence is that of human Fms-like tyrosine kinase (Flt-3 ligand). The invention is directed to enhancing the
                                Claim 2; Page 137-138; 149pp; English.
                                                                                                                                                                                          30-JUL-1999;
                                                                                                                                                                                                               31-JUL-2000;
                                                                                                                                                                                                                                       08-FEB-2001.
                                                                                                                                                                                                                                                                                            Domain
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                                                                                                                                                                                                                                                                                                                                                                                 Peptide
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                                                                                                              2001-123319/13.
DB; AAF30312.
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                                                                                                                                                                                          99US-0146170
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                                                                                                                                                                                                                                                                                                                                                          /label=
27..235
                                                                                                                                                                                                                                                                                           /label= Transmembrane_domain
206..235
                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                              /label= Cytoplasmic_domain
                                                                                                                                                                                                                                                                                                                        /label= Extracellular_domain
                                                                                                                                                                                                                                                                                                                                              /label= Mature_protein
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L.8e-108;
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Best Local Similarity
Matches 234; Conserv
                                                                                                                                                                                                                                                   Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                 cell surface tyrosine kinase receptor; hematopoletic prografio celevillar expansion; cellular differentiation; natural killer cell; cancer; dendritic cell; immune response; autoimmunity; immunosuppromyelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblas
                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV; neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy; cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
                        02-JUL-1998;
                                                                               25-JUN-1999;
                                                                                                                                         13-JAN-2000
                                                                                                                                                                                                  WO200001823-A2
                                                                                                                                                                                                                                                                                                                                            multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human flt-3 mutein L-3H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       compositions comprising the polynucleotides are useful for suppressing tumour growth in a mammal. The tumour is melanoma, glioma or lymphoma, particularly B-cell lymphoma. They can also be used for the prophylactic and/or therapeutic treatment of: (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis and C in humans), parasitic (e.g. malaria) and fungal infections (b) autoimmune diseases (e.g. rheumatoid arthritis and osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs. Various other examples of these diseases are given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY69721 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the fit 3 ligand. The polynucleotides are incorporated into the cells of the vertebrate in vivo, and a prophylactically or therapeutically effective amount of Fit 3 ligand and I or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immune response of a vertebrate to an antigen or a cytokine by administering in vivo, into a tissue of a vertebrate, a Flt-3 ligand-encoding polynucleotide, and 1 or more antigen- or cytokine-encoding polynucleotides. The Flt-3 ligand-encoding polynucleotide may encode the present full-length human Flt-3 ligand polypeptide, or amino acids 27-185, 1-185, 27-235 or 1-235 for 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ligand polypof the Flt-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RFVQTNISRLLQETSEQLVALKFWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTBIHFVTKCAFQPPPSCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTVLAPAWSPTTYLLLLLLLSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPYTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APQPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASNLQDEELCGALWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV
                                                                                                                                                                                                                                                                                                                                            myeloma; leukemia; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                        98US-0109100
                                                                               99WO-US14296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1236;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infections;
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RRESULT 9
AAM69007
ID AAM64
XX AAM6
AC AAM6
XX AAM6
XX Huma
XX Huma
KW Huma
KW Grug
KW Cong
KW Cong
KW Grug
KW Gen
XX Home
XX Home
XX WO98
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                                                                                                                                                                                                                                                                                                                                                                                                                             δð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              colony stimulating factors or protein kinases. The protein can also modulate, augment or enhance a patient's immune response and can be used to treat an immune disorder (e.g. allergy, autoimmunity or immunosuppression). The protein may be used to treat a pathological condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast, small cell lung, testicular or ovarian cancer, lymphoma, multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the full length wild type (AAY69719) or mature (AAY69720) flt3-L polypeptides. This sequence represents an example of the novel flt-3 ligands and comprises the L-3H mutant polypeptide. The flt3-L protein binds cell surface tyrosine kinase receptors and regulate growth and differentiation of hematopoletic progenitor cells. The flt3-L protein can be used to induce cellular expansion (especially in vivo) or dendritic differentiation, e.g. in hematopoletic, natural killer (NK) or dendritic cells, especially in the presence of growth factors such as interleukins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mutant soluble flt3 ligand polypeptide used in cellular expansion, immune response stimulation or treatment of pathological conditions contains amino acid substitutions at positions 8, 84, 118 or 122 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides which exhibits increased or decreased biological activity relative to the full length wild type (AAY69719) or mature (AAY69720) flt3-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Graddis TJ,
                  WO9818923-A1
                                                    Homo sapiens.
                                                                                                       bone marrow reconstitution; haematological disease; immune deficiency; drug-induced myelosuppression; renal dialysis; gene therapy; infection congenital metabolic disease; neurological disease; therapy;
                                                                                                                                                                                                   Human flt-3
                                                                                                                                                                                                                                     01-OCT-1998
                                                                                                                                                                                                                                                                       AAW69007;
                                                                                                                                                                                                                                                                                                         AAW69007 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                        dendritic cell
                                                                                                                                                                                                                                                                                                                                                                                                   182
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                                                                                                                                                                                                                                                                                                                                                                                                   LHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH
                                                                                                                                                                                                                                                                                                                                                                                                                  LHWQRTRRRTPRPGEQVPPVPSPQDLLLLVEH 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ITRONFSRCLELOCOPDSSTLPPPWSPRPLEATAPTAPOPPLLLLLLLLPVGLLLLAAAWC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLLPVGLLLLAAAWC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKFW 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWME 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211;
                                                                                                                                                              flt-3 receptor agonist; haematopoietic cell stimulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neuroblastoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212 AA;
                                                                                                                                                                                               receptor agonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McGrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79-80; 90pp; English.
                                                                                        production
                                                                                                                                                                                                                                                                                                         peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.5%;
100.0%;
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                                                                                                                                                                                                                                                                                                           209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1124; DB 21;
Pred. No. 5.9e-98;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                   212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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This sequence represents a rearranged human flt-3 receptor agonists of CC the invention. The agonists have a modified flt-3 ligand amino acid CC sequence. The agonists are used to stimulate production of haematopoietic CC cells in vivo (e.g. in a subject about to donate blood) or for ex vivo CC expansion for subsequent transplantation, e.g. to reconstitute bone CC marrow after chemotherapy, disease etc., or to treat haematological CC disease such as drug-induced myelosuppression, defects caused by CC infections, burns or renal dialysis. Optionally ex vivo expanded cells CC are transduced with a gene therapy vector for treating e.g. congenital CC metabolic diseases, immune deficiency, neurological disease, cancer and CC infections. The agonists can also be used in the treatment of tumours, CC infections and autoimmune disease, when administered optionally with an CC antigen. The agonist can also be used in the production of dendritic CC cells for use as an immunising adjuvant for treatment disorders including acquired immune deficiency syndrome. Compared with native ligands, the CC may agonists have better stimulatory activity, reduced side effects CC and/or better physical properties such as solubility, stability or refold CC efficiency. When used together with other stimulatory agents, the
                Query Match
Best Local (
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rearranged flt-3 receptor agonists and nucleic acids encoding them used to stimulate production of haematopoietic and dendritic cells, for treatment of haematological diseases, bone marrow reconstitution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staten NR, Streeter PR,
                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 9-10; 158pp; English
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                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McKearn JP,
                                                                             209 AA;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97WC-US18700
                89.7%; Score 1114; DB 19; 100.0%; Pred. No. 5.1e-97;
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R, Woulfe
  0,
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  Mismatches
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  0;
                                     Length 209;
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RESULT 10
AAY69720
ID AAY69
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                             05-JUL-2000
                                                 AAY69720;
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                                                                                                                                                                                        147
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                                                                                                                          WORTERFIPERPGEOVPPVPSPQDLLLVEH
                                                                                                                                              WQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235
                                                                                                                                                                              RQNFSRCLELQCQFDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLLPVGLLLLAAAWCLH
                                                                                                                                                                                                            KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT
                                                                                                                                                                                                                       KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT
                                                                                                                                                                                                                                                     TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL
                                                                                                                                                                   RQNFSRCLELQCQFDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLLPVGLLLLAAAWCLH
                                                                       standard;
                             (first entry)
                                                                       Protein;
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                                                                       ĄΑ
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                                                                                                                                                                     180
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0

Mature wild type human flt-3 protein

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The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides which exhibits increased or decreased biological activity relative to the full length wild type (AAX69719) or mature (this sequence) flt3-L colypeptides. The flt3-L protein binds cell surface tyrosine kinase creeptors and regulate growth and differentiation of hematopoietic progenitor cells. The flt3-L protein can be used to induce cellular cells expansion (especially in vivo) or differentiation, e.g. in chematopoietic, natural killer (NK) or dendritic cells, especially in the presence of growth factors such as interleukins, colony stimulating cellscrors or protein kinases. The protein can also modulate, sugment or cenhance a patient's immune response and can be used to treat an immune cellscropy, autolumunity or immunosuppression). The protein can also modulate, sugment or constant canemia, HIV infection, breast, small cell lung, testicular or lankemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mutant soluble flt3 ligand polypeptide used in cellular expansion, immune response stimulation or treatment of pathological conditions contains amino acid substitutions at positions 8, 84, 118 or 122 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell surface tyrosine kinase receptor; hematopoietic progenitor cell; cellular expansion; cellular differentiation; natural killer cell; cencer; dendritic cell; immune response; autoimmunity; immunosuppression; myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 89-90; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  multiple myeloma; leukemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV; neuroprotective; antiallergic; flt3 ligand, flt3-L; wild type; allergy;
     181
                                                             207
                                                                                                                  121
                                                                                                                                                                      147
                                                                                                                                                                                                                              61
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                                                                                                                                                                                                                                                                                                                                                                                                  27
                                WQRTRRRTPRPGEQVPPVPSPQDLLLVEH
                                                                                                                                                                                                                                                                                                                                                            TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL
WQRTRRRTPRPGEQVPPVPSPQDLLLVEH
                                                                                                      RQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWCLH
                                                                                                                                   RONFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWCLH
                                                                                                                                                                                                               KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT
                                                                                                                                                                                                                                                     KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT
                                                                                                                                                                                                                                                                                                                            TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000-182115/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.7%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1114; DB 21; Pred. No. 5.1e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                    235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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RESULT 11 AAY69723

Qy

147

RONFSRCLELQCOPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWCLH

KTVAGSKMQGLLERVNTEIHFVTECAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT 120

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Qy DЪ Qy Ъ δÃ 망 δÔ

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Qy
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Best Local
                                                                                                                                                                                                                       be used to induce cellular expansion (especially in vivo) or differentiation, e.g. in hematopoletic, natural killer (NK) or dendritic cells, especially in the presence of growth factors such as interleukins, colony stimulating factors or protein kinases. The protein can also modulate, augment or enhance a patient's immune response and can be used to treat an immune disorder (e.g. allergy, autoimmunity or immunosuppression). The protein may be used to treat a pathological condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast, small cell ling, testicular or ovarian cancer, lymphoma, multiple
                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                        polypeptides. This sequence represents an example of the novel flt-3 ligands and comprises the K84E mutant polypeptide. The flt3-L protein binds cell surface tyrosine kinase receptors and regulate growth and differentiation of hematopoietic progenitor cells. The flt3-L protein can
                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides which exhibits increased or decreased biological activity relative to the full length wild type (AAY69719) or mature (AAY69720) flt3-L
                                                                                                                                                                                                                  myeloma, neuroblastoma or acute leukemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-182115/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mutant soluble flt3 ligand polypeptide used in cellular expansion, immune response stimulation or treatment of pathological conditions contains amino acid substitutions at positions 8, 84, 118 or 122 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Graddis TJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUL-1998;
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV; neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy; cell surface tyrosine kinase receptor; hematopoletic progenitor cell; cellular expansion; cellular differentiation; natural killer cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY69723 standard; Protein;
                  87
                                                                                      27
                                                               TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL
KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT 146
                                                TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL
                                                                                                                     208;
                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                myeloma;
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                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McGrew JT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90pp; English
                                                                                                                                 9.4%;
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                                                                                                                                 Score 1110;
Pred. No. 1
                                                                                                              Mismatches
                                                                                                          0;
                                                                                                                                             Length
                                                                                                               Indels
                                                                                                                                             209;
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RESULT 12
AAY69726
ID AAY69
XX AAY69726
XX AAY69
XX AAY69
XX AAY69
XX Immu
KW Ineur
KW Cell
KW INEU
KW INUL
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Matches
                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV; neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy; cell surface tyrosine kinase receptor; hematopoietic progenitor cell; cellular expansion; cellular differentiation; natural killer cell; cancer; dendritic cell; immune response; autoimmunity; immunosuppression; myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
                                                                                                                                                                                                                                                                                                                                                                                     polypeptides. This sequence represents an example of the novel flt-3 ligands and comprises the Q122R mutant polypeptide. The flt3-L protein binds cell surface tyrosine kinase receptors and regulate growth and differentiation of hematopoietic progenitor cells. The flt3-L protein can be used to induce cellular expansion (especially in vivo) or differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic cells, especially in the presence of growth factors such as interleukins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides which exhibits increased or decreased biological activity relative to the full length wild type (AAX69719) or mature (AAX69720) flt3-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Graddis TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-JUL-1998;
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                                                                                                                      Sequence
                                                                                                                                                                                                            immunosuppression). The protein may be used to treat a pathological condition e.g. myelodysplasia, aplastic anemia, HIV infection, brea small cell lung, testicular or ovarian cancer, lymphoma, multiple
                                                                                                                                                                                                                                                                                                  modulate, augment or enhance a patient's immune response and can to treat an immune disorder (e.g. allergy, autoimmunity or
                                                                                                                                                                                                                                                                                                                                                                  colony stimulating factors or protein kinases. The protein can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IMMV ) IMMUNEX CORP
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                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000-182115/16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WQRTRRRTPRPGEQVPPVPSPQDLLLVEH 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WQRTRRRTPRPGEQVPPVPSPQDLLLVEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 soluble flt3 ligand polypeptide used in cellular expansion, response stimulation or treatment of pathological conditions ns amino acid substitutions at positions 8, 84, 118 or 122 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 88-89;
                                                                                                                                                                                      neuroblastoma
                                                                                                                         209 AA
   Conservative
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                            89.4%;
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Score 1110; D
Pred. No. 1.2e
1; Mismatches
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                                                                                                                                                                                         leukemia
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Gaps
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RESULT 13
AAY69727
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                                                                        polypeptides. This sequence represents an example of the novel flt-3 ligands and comprises the L26F mutant polypeptide. The flt3-L protein binds cell surface tyrosine kinase receptors and regulate growth and differentiation of hematopoietic progenitor cells. The flt3-L protein can be used to induce cellular expansion (especially in vivo) or differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic cells, especially in the presence of growth factors such as interleukins, colony stimulating factors or protein kinases. The protein can also
                                                                                                                                                                                                                                                                                                               Mutant soluble flt3 ligand polypeptide used in cellular expansion, immune response stimulation or treatment of pathological condition contains amino acid substitutions at positions 8, 84, 118 or 122 \,
                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                             The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides which exhibits increased or decreased biological activity relative to the full length wild type (AAY69719) or mature (AAY69720) flt3-L
                                                                                                                                                                                                                                                                              Claim 13; Page 82-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
myclodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell surface tyrosine kinase receptor; hematopoietic progenitor cell; cellular expansion; cellular differentiation; natural killer cell;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                multiple myeloma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human flt-3 mutein L26F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY69727 standard;
                             to treat an immune disorder (e.g. allergy, autoimmunity or immunosuppression). The protein may be used to treat a pathological
                                                               modulate, augment or enhance a patient's immune response and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMUNEX CORP.
               e.g. myelodysplasia, aplastic anemia,
                                                                                                                                                                                                                                                                                                                                                                                                                   McGrew JT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0109100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US14296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunosuppressive; cytostatic; antianemic; anti-HIV;
antiallergic; flt3 ligand; flt3-L; wild type; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mutein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  209
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                  HIV infection,
                                                                                                                                                                                                                                                                                                                    conditions
3 or 122 -
                    breast,
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RESULT 14
AAY69729
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The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides which exhibits increased or decreased biological activity relative to the full length wild type (AAX69719) or mature (AAX69720) flt3-L polypeptides. This sequence represents an example of the novel flt-3 ligands and comprises the L26F mutant polypeptide. The flt3-L protein binds cell surface tyrosine kinase receptors and regulate growth and differentiation of hematopoietic progenitor cells. The flt3-L protein car
                                                                                                                         Claim 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV; neuroprotective; antiallergic; fit3 ligand; fit3-L; wild type; allergy; cell surface tyrosine kinase receptor; hematopoietic progenitor cell; cellular expansion; cellular differentiation; natural killer cell; cancer; dendritic cell; immune response; autoimmunity; immunosuppression; myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma; myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
                                                                                                                                                   contains amino
                                                                                                                                                                                                                                                                 (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                               02-JUL-1998;
                                                                                                                                                                                                                                                                                                                          25-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                       13-JAN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                       multiple
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY69729 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLLPVGLLLLAAAWCLH 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT
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                                                                                                                                        soluble flt3 ligand polypeptide used in cellular expansion, response stimulation or treatment of pathological conditions amino acid substitutions at positions 8, 84, 118 or 122 -
                                                                                                                                                                                                                                       ТJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       myeloma;
                                                                                                                      Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neuroblastoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mutein
                                                                                                                                                                                                                                       McGrew
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                                                                                                                        78-79;
                                                                                                                                                                                                                                                                                               98US-0109100
                                                                                                                                                                                                                                                                                                                        99WO-US14296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     leukemia; mutein
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99.5%;
                                                                                                                  90pp; English.
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Pred. No. 1.2e-96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       209;
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RESULT 15
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                          cell surface tyrosine kinase receptor; hematopoietic progenitor cell; cellular expansion; cellular differentiation; natural killer cell; cancer; dendritic cell; immune response; autoimmunity; immunosuppression; myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
                                                                                                                                                        02-JUL-1998;
                                                                                                                                                                                                                                             WO200001823-A2
                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                multiple myeloma; leukemia; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY69722 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     be used to induce cellular expansion (especially in vivo) or differentiation, e.g. in hematopoletic, natural killer (NK) or dendritic cells, especially in the presence of growth factors such as interleukins, colony stimulating factors or protein kinases. The protein can also modulate, augment or enhance a patient's immune response and can be used to treat an immune disorder (e.g. allergy, autoimmunity or
                                                                                                                                                                                     25-JUN-1999;
                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                           neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                       Immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Human flt-3 mutein H8Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  condition e.g. myelodysplasia, aplastic a small cell lung, testicular or ovarian ca myeloma, neuroblastoma or acute leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunosuppression). The protein may be used to treat a pathological condition e.g. myelodysplasia, aplastic anemia, HIV infection, brea small cell lung, testicular or ovarian cancer, lymphoma, multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                    2000-182115/16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KTVTGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT
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                                                                                              McGrew
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                                                                                                                                                                                                                                                                                                                                                                                  immunosuppressive; cytostatic; antianemic; anti-HIV;
antiallergic; flt3 ligand; flt3-L; wild type; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.4%;
99.5%;
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Pred. No. 1.2e-96;
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Mutant soluble flt3 ligand polypeptide used in cellular expansion, immune response stimulation or treatment of pathological condition contains amino acid substitutions at positions 8, 84, 118 or 122

Claim 4; Page 81-82; 90pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to novel soluble flt3 ligand (flt3-L) polypoptides cc which exhibits increased or decreased biological activity relative to cc the full length wild type (AAX69719) or mature (AAX69720) flt3-L cc polypoptides. This sequence represents an example of the novel flt-3 cc ligands and comprises the H8Y mutant polypoptide. The flt3-L protein cc binds cell surface tyrosine kinase receptors and regulate growth and cc differentiation of hematopoietic progenitor cells. The flt3-L protein can be used to induce cellular expansion (especially in vivo) or cc differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic cc lls, especially in the presence of growth factors such as interleukins, cc colony stimulating factors or protein kinases. The protein can also cc modulate, augment or enhance a patient's immune response and can be used to treat an immune disorder (e.g. allergy, autoimmunity or condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast, cm myeloma, neuroblastoma or acute leukemia.
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Search completed: November 24, 2002, 10:10:12 Job time : 32.7704 secs
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Best Local Similarity 99.5%;
Matches 208; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                             181 WORTRRTPRPGEQVPPVPSPQDLLLVEH 209
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                                                                                                                                                                                                                                                                    87
                                                                                                                                                                                                                                                                                                      WQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235
                                                                                                                                                                                                                              KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                           209 AA;
                                                                                                                                                                                                                                                                                                                                                                                  Score 1108; DB 21; Length 209;
Pred. No. 1.9e-96;
1; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB Maximum DB Database Run OM protein - protein search, using sw model Total number of hits satisfying chosen parameters: Searched: Scoring table: Perfect score: Title: 900 seq length: 0
seq length: 2000000000 10: 11: 12: 13: Gapop 10.0 , Gapext 0.5 BLOSUM62 1 MTVLAPAWSPTTYLLLLLLL......RPGEQVPPVPSPQDLLLVEH 235 US-09-448-378-1 1242 100480 seqs, 15661496 residues November 24, '/cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
'/cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
'/cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
'/cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
'/cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
'/cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
'/cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
'/cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
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'/cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*
'/cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\* Published\_Applications\_AA: \* 2002, 10:11:46; Search time 8.57296 Seconds (without alignments) 429.309 Million cell updates/se 100480 cell updates/sec

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

19	18	17	16	15	14	13	12	11	10	. 9	00	7	6	ı U	4 1	٠ لـ			Result No.
506.5	768.5	768.5	768.5	1100	1106	1107	1108	1108	1110	1110	1110	1110	1114	1124	1242	1242	1242	1242	Score
40.8	61.9	61.9	61.9	88.6	89.0	89.1	89.2	89.2	89.4	89.4	89.4	89.4	89.7	90.5	100.0	100.0	100.0	100.0	Query Match I
137	231	231	231	209	209	209	209	209	209	209	209	209	209	212	235	235	235	235	Length
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US-09-904-536-19	US-09-983-806-2	US-09-448-378-2	US-10-095-449-2	US-09-904-536-16	US-09-904-536-8	US-09-904-536-13	US-09-904-536-15	US-09-904-536-11	US-09-904-536-17	US-09-904-536-14	US-09-904-536-12	US-09-904-536-9	US-09-904-536-18	US-09-904-536-10	US-09-904-536-1	US-09-983-806-6	US-09-448-378-1	US-10-095-449-6	ID
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## ALIGNMENTS

RESULT 1 US-10-095-449-6 Sequence 6, Application US/10095449 Patent No. US20020160004A1 GENERAL INFORMATION: COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/095,449
FILING DATE: 13-Mar-2002
CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION: PRIOR APPLICATION DATA: APPLICANT: Lyman, Stewart D.

Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS: APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/068,394
FILING DATE: MAY 24, 1993 CITY: Seattle STATE: Washington COUNTRY: US APPLICATION NUMBER: 08/6 FILING DATE: 24-JUN-1996 ADDRESSEE: Stephen L. STREET: 51 University 08/669,692 Malaska, Street Version #5.1 Immunex Corporation

TELEFAX: (206)

233-0644

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US-09-448-378-1
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Best Local Similarity
Matches 235; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09448378 Patent No. US20020034517A1
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 2836-D
CURRENT APPLICATION NUMBER: US/09/448,378
CURRENT FILING DATE: 199-11-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Brasel, Kenneth
TITLE OF INVENTION: Dendri
                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 235
TYPE: PRT
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
181
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APQPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235
             APQPPLLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235
                                                              RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT
                                                                                RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT 180
                                                                                                                                                                                                               MTVLAPAWSPTTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
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Pred. No. 2e-103;
Mismatches 0
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Pred. No. 2e-103;
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RESULT 3

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RESULT

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US-09-983-806-6
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Best Local
                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
181
                      181 APQPPLLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235
                                                                                 121
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                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                  1 MTVLAPAWSPTTY1LLLLLLSGGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV
                                                                                                                                                                                                                                                                                            1 MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lyman, Stewart D.

Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                     RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT
                                                                                                                                                                  ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL
                                                                                                                                                                                        ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL
APQPPLLLLLLPVGLLLLAAAWCLHWQRTRRTPRPGEQVPPVPSPQDLLLVEH
                                                                                 RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Apple Macintosh OPERATING SYSTEM: Macintosh 7.0.1 SOFTWARE: Microsoft Word, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 235 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 32, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Malaska, Stephen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 0 FILING DATE: 03-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/444,626 FILING DATE: 19-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 25-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 51 University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Stephen L.
                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1242; DB 1 100.0%; Pred. No. 2e-103;
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                                                                                                                                                                                                                                                     SEQ ID NO 10
LENGTH: 212
                                                                                                                                         Matches
                                                                                                                                                        Query Match
Best Local
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Patent No. US200201111475A1
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Best Local Similarity
Matches 235; Conserv
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
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CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.1
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TYPE: PRT
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               RLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPW 144
                                                                               SGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWME 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT
RLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPW
                                                               SGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWME
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Pred. No. 2e-103;
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; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-9
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US-09-904-536-9
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APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
APPLICANT: MCGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
                                                                SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 9
                                                                                                                                                                                                                                                                Sequence 9, Application US/09904536 Patent No. US20020111475A1
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
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                                                                                                              PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100 PRIOR FILING DATE: 1999-07-02
                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/904,536 CURRENT FILING DATE: 2001-07-16
                                                                                                NUMBER OF SEQ ID NOS: 20
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TYPE: PRT
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es 209; Conserv
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US-09-904-536-14
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Best Local S
Matches 208
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGIH: 209
           GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE GEFERENCE: 03560.0028
CURREN APPLICATION NUMBER: US/09/904,536
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APPLICANT: McGrew, Jeffrey T.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-1 MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/904,536
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Pred. No. 9.3e-92;
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Pred., No. 9.3e-92;
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US-09-904-536-17
Sequence 17, Application US/09904536
Patent No. US20020111475A1
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
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Best Local Similarity
Matches 208; Conserv
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LENGTH: 209
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PRIOR APPLICATION NUMBER: PRIOR /
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
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TYPE: PRT
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TYPE: PRT
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WQRTRRRTPRPGEQVPPVPSPQDLLLVEH
               WQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235
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Pred. No. 9.3e-92;
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Pred. No. 9.3e-92;
1; Mismatches 0
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RESULT 12
US-09-904-536-15
US-09-904-536-15
Sequence 15, Application US/09904536
Patent No. US20020111475A1
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: MCGrew, Jeffrey T.
FITHE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260,0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
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APPLICANT: McGrew, Jeffrey T.
APPLICANT: McGrew, Jeffrey T.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: ELT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR EILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
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PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
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TYPE: PRT
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ORGANISM: Homo sapiens
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Pred. No. 1.4e-91;
1; Mismatches 0;
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Pred. No. 1.4e-91;
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US-09-904-536-13
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US-09~904-536-8
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SEQ ID NO 13
LENGTH: 209
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                                SEQ ID NO 8
LENGTH: 209
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Best Local (
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APPLICANT: McGrew, Jeffrey T.
APPLICANT: McGrew, Jeffrey T.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLI3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR APPLICATION NUMBER: PROPOSED OF SEQ ID NOS: 20
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                            APPLICANT: Graddis, Thomas J.
APPLICANT: MCGrew, Jeffrey T.
TITLE OF INVENTION: FLI3-I. MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
                                                                                    PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100 PRIOR FILING DATE: 1999-07-02 NUMBER OF SEQ ID NOS: 20
                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/904,536 CURRENT FILING DATE: 2001-07-16
                                                                     SOFTWARE: PatentIn Ver. 2.1
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ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
                   TYPE: PRT
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PRIOR APPLICATION UNMBER: 2001-07-16
PRIOR FILING DATE: 2001-07-16
PRIOR FILING DATE: 1999-07-02
INUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENCTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
US-09-904-536-16
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; Sequence 16, Application US/09904536
; Patent No. US20020111475A1
; GENERAL INFORMATION:
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Matches 208
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE 03260.0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
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